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Ala	Gln	Pro	500	Thr	Ser	Asp	Ala	505	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala	Asp
		515					520						525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535						540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Ala	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595				600						605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 290

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 598 GCA

&lt;400&gt; 290

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75				80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155				160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195					200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					

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Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Ala	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 291

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 598 GAC

&lt;400&gt; 291

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu



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290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Asp Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620

&lt;210&gt; 292

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 598 GAC

&lt;400&gt; 292

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70

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Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170						175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Asp	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 293

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 598 AGC

&lt;400&gt; 293

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu

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				85				90					95				
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
		130				135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145				150						155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165						170					175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
			180					185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225				230						235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245						250					255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265					270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305				310						315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			325						330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
			340					345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405						410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420				425						430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465				470						475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545				550						555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                   580                  585                  590  
 Ile His His Ile Met Ser Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
                   595                  600                  605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
           610                  615                  620

&lt;210&gt; 294

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 598 AGC

&lt;400&gt; 294

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                   180                  185                  190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                   195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
   305                  310                  315                  320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
                   325                  330                  335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                   340                  345                  350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

		355					360				365					
Ile	His	His	Ile	Met	Ser	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
	370					375					380					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
385					390					395						
<210>	295															
<211>	621															
<212>	PRT															
<213>	Artificial Sequence															
<220>																
<223>	Mutant rep protein: rep78 600 GCG															
<400>	295															
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1			5						10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
			20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
			85						90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
			165					170					175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225				230						235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			245						250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr						

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Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
370						375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
450						455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
530						535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Ala	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
610						615					620				

&lt;210&gt; 296

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 600 GCG

&lt;400&gt; 296

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
50						55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
130						135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala

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145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170						175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235						240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290				295						300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310						315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325					330						335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340					345					350			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
	355					360					365				
Ile	His	His	Ile	Met	Gly	Lys	Ala	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370			375						380					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390				395						

&lt;210&gt; 297

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant -rep protein: rep78 600 CCG

&lt;400&gt; 297

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
	35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65				70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
		85					90						95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
	100						105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
	115				120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130				135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150				155						160



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Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500				505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580				585						590		
Ile	His	His	Ile	Met	Gly	Lys	Pro	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 298

&lt;211&gt; 397

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 600 CCG

&lt;400&gt; 298

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Pro Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 299

&lt;211&gt; 621

&lt;212&gt; PRT

-351-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 601 GCA

&lt;400&gt; 299

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

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		435				440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Ala	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

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<210> 300
<211> 397
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Mutant rep protein: rep52 601 GCA

<400>	300															
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			35				40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
50					55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
130						135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					

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Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Ala	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370				375						380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 301

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 78 335 420 495 GCT GCC GCC

&lt;400&gt; 301

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys

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225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250				255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265				270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355						360					365		Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					Val
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420					425					430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala
				485				490						Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
545					550				555					Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
				565					570					Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
			580					585					590	Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
		595					600					605		Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
	610					615					620			

&lt;210&gt; 302

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 335 420 495 GCT GCC GCC

&lt;400&gt; 302

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	

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Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
	50				55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85						90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130				135						140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
					165				170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210				215						220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	290					295					300					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
305					310					315					320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
				325					330					335		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
			340					345					350			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
		355					360					365				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
	370					375					380					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
385					390					395						

&lt;210&gt; 303

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 335 420 495 GCT GCC GCC

&lt;400&gt; 303

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1			5						10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	



			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370														

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           515                                  520          525  
 Arg Leu Ala Arg Gly His Ser Leu  
           530                                  535

<210> 304  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 335 420 495 GCT GCC GCC

<400> 304  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
           20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
           35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
           50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
           85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala  
           100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
           115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
           130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
           165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
           180                  185                  190  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
           195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
           210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
           245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
           260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
           275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
   305                                  310

<210> 305  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>

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&lt;223&gt; Mutant rep protein: rep78 39 140 GCA GCC

&lt;400&gt; 305

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Ala	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150				155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310				315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				

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Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515				520						525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580				585						590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595				600						605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 306

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 39 140 GCA GCC

&lt;400&gt; 306

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Ala	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35				40						45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115				120						125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala

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				245					250					255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265					270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290				295						300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			325						330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		340						345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
370					375						380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385				390						395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		420					425						430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	435					440						445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
450					455						460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465				470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500					505						510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	515				520							525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
530					535												

&lt;210&gt; 307

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 279 428 451 GCC GCT GCC

&lt;400&gt; 307

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
		20					25					30					
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
	35				40						45						
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50				55					60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65				70				75						80			
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
			85					90					95				
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
		100					105						110				

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Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Ala	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Ala	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp

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      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

<210> 308
<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant rep protein:  rep52  279 428 451 GCC GCT
      GCC

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Gln	Trp	Ile	Gln 20	Glu	Asp	Gln	Ala	Ser 25	Tyr	Ile	Ser	Phe	Asn 30	Ala	Ala	
Ser	Asn 35	Ser	Arg	Ser	Gln	Ile	Lys 40	Ala	Ala	Leu	Asp 45	Asn	Ala	Gly	Lys	
Ile	Met 50	Ser	Leu	Thr	Lys	Ala 55	Ala	Pro	Asp	Tyr	Leu 60	Val	Gly	Gln	Gln	
Pro 65	Val	Glu	Asp	Ile	Ser 70	Ser	Asn	Arg	Ile	Tyr 75	Lys	Ile	Leu	Glu 80	Leu	
Asn	Gly	Tyr	Asp 85	Pro	Gln	Tyr	Ala	Ala 90	Ser	Val	Phe	Leu	Gly 95	Trp	Ala	
Thr	Lys	Lys	Phe 100	Gly	Lys	Arg	Asn 105	Thr	Ile	Trp	Leu	Phe 110	Gly	Pro	Ala	
Thr	Thr 115	Gly	Lys	Thr	Asn	Ile 120	Ala	Glu 125	Ala	Ile	Ala	His 130	Thr	Val	Pro	
Phe	Tyr 135	Gly	Cys	Val	Asn 140	Trp	Thr	Asn 145	Glu	Asn 150	Phe 155	Pro	Phe	Asn	Asp	
Cys 160	Val	Asp	Lys	Met 165	Val	Ile	Trp	Trp 170	Glu	Glu 175	Gly	Lys	Met	Thr	Ala	
Lys	Val	Val	Glu 180	Ser	Ala	Lys	Ala 185	Ile	Leu 190	Gly	Gly	Ser	Lys 195	Val	Arg	
Val	Asp	Gln	Lys 195	Cys	Lys	Ser	Ser 200	Ala	Gln	Ile	Asp 205	Pro	Thr 210	Pro	Val	
Ile	Val 215	Thr	Ser	Asn	Thr	Asn	Met 220	Cys	Ala	Val	Ala 225	Asp	Gly	Asn	Ser	
Thr	Thr 230	Phe	Glu	His	Gln	Gln	Pro 235	Leu	Gln	Asp	Arg 240	Met	Phe	Lys	Phe	
Glu 245	Leu	Ala	Arg	Arg	Leu	Asp	His 250	Asp	Phe	Gly 255	Lys	Val	Thr	Lys	Gln	
Glu	Val	Lys	Asp 260	Phe	Phe	Arg	Trp 265	Ala	Lys	Asp	His 270	Val	Val	Glu 275	Val	
Glu	His	Glu	Phe 280	Tyr	Val	Lys	Lys 285	Gly	Gly	Ala	Lys 290	Lys	Arg	Pro	Ala	
Pro	Ser 295	Asp	Ala	Asp	Ile	Ser	Glu 300	Pro	Lys	Arg	Val 305	Arg	Glu	Ser	Val	
Ala	Gln 310	Pro	Ser	Thr	Ser	Asp 315	Ala	Glu	Ala	Ser 320	Ile	Asn	Tyr	Ala	Asp	
Arg 325	Tyr	Gln	Asn	Lys	Cys 330	Ser	Arg	His	Val	Gly 335	Met	Asn	Leu	Met	Leu	
Phe	Pro	Cys	Arg 340	Gln	Cys	Glu	Arg 345	Met	Asn 350	Gln	Asn	Ser	Asn 355	Ile	Cys	
Phe	Thr	His	Gly 355	Gln	Lys	Asp	Cys 360	Leu	Glu	Cys	Phe 365	Pro	Val	Ser	Glu	
Ser	Gln 370	Pro	Val	Ser	Val	Val	Lys 375	Lys	Ala	Tyr	Gln	Lys 380	Leu	Cys	Tyr	
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	



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370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 309  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 279 428 451 GCC GCT  
 GCC

<400> 309  
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 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410						415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Ala	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

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<220>
<223> Mutant rep protein: rep40 279 428 451 GCC GCT GCC
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Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Ala	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
50						55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65				70						75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85						90				95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
130						135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145				150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser	
		195				200						205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210				215						220					
Glu	Leu	Ala	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225				230						235					240	

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305                  310

&lt;210&gt; 311

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 125 237 600 GCG GCC GCG

&lt;400&gt; 311

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1                  5                  10                  15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                  25                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                  40                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
                   50                  55                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65                  70                  75                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                  90                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                  105                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu  
                   115                  120                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
                   130                  135                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145                  150                  155                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                  170                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                  185                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                  200                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
                   210                  215                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys  
 225                  230                  235                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   245                  250                  255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys  
                   260                  265                  270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   275                  280                  285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   290                  295                  300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305                  310                  315                  320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

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          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610          615          620

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&lt;210&gt; 312

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 125 237 600 GCG GCC GCG

&lt;400&gt; 312

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
    115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
    165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
    180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
    195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
    245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
    260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
    275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
    325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
    340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
    355      360      365
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
    370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 313

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 125 237 600 GCG GCC GCG

&lt;400&gt; 313

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
    20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
    35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
    85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
    100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu

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Pro	Asn	115	Trp	Phe	Ala	Val	Thr	120	Lys	Thr	Arg	Asn	Gly	125	Ala	Gly	Gly	Gly
	130							135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
				165					170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
		180						185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Ala	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		260						265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325				330						335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
		340					345					350						
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
	355					360					365							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370				375					380								
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
				405				410					415					
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
		420					425					430						
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455				460								
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
				485				490					495					
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
		500					505					510						
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 314

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 125 237 600 GCG GCC GCG

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<400> 314  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 315

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 163 259 GCT GCG

&lt;400&gt; 315

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80



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Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu

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				565					570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 316

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 163 259 GCT GCG

&lt;400&gt; 316

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5					10					15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70				75						80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115				120						125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130				135				140								
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145				150					155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215					220							
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225				230					235					240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290				295						300						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
305				310					315					320			
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
			325					330						335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
		340					345						350				

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 317  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 163 259 GCT GCG

<400> 317  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

[illegible]

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<220>
<223> Mutant rep protein: rep40 163 259 GCT GCG
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<400> 318																
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
50					55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70						75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
130						135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
210						215					220					

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 319

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 17 127 189 GCG GCT GCG

&lt;400&gt; 319

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360					365		Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420					425					430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490						Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500				505						510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520						525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
545					550					555				Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			565						570					Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
			580					585					590	Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	595						600					605		Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615				620				

&lt;210&gt; 320

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 17 127 189 GCG GCT GCG

&lt;400&gt; 320

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Ala	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20					25						30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90						95	

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Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Ala	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150						155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Ala	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 321

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 350 428 GCT GCT

&lt;400&gt; 321

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln

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450		455		460
Glu Val Lys Asp Phe	Phe Arg Trp Ala Lys Asp	His Val Val Glu Val		
465	470	475		480
Glu His Glu Phe Tyr	Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala			
	485	490		495
Pro Ser Asp Ala Asp	Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val			
	500	505		510
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp			
	515	520		525
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly Met Asn Leu Met Leu			
	530	535		540
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln Asn Ser Asn Ile Cys			
545	550	555		560
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys Phe Pro Val Ser Glu			
	565	570		575
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr			
	580	585		590
Ile His His Ile Met Gly	Lys Val Pro Asp Ala Cys Thr Ala Cys Asp			
	595	600		605
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe Glu Gln			
610	615	620		

&lt;210&gt; 322

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 350 428 GCT GCT

&lt;400&gt; 322

Met Glu Leu Val Gly Trp Leu Val	Asp Lys Gly Ile Thr Ser Glu Lys
1	15
Gln Trp Ile Gln Glu Asp Gln Ala	Ser Tyr Ile Ser Phe Asn Ala Ala
	20
Ser Asn Ser Arg Ser Gln Ile Lys	Ala Ala Leu Asp Asn Ala Gly Lys
	25
Ile Met Ser Leu Thr Lys Thr Ala	Pro Asp Tyr Leu Val Gly Gln Gln
	30
Pro Val Glu Asp Ile Ser Ser Asn	Arg Ile Tyr Lys Ile Leu Glu Leu
	35
Asn Gly Tyr Asp Pro Gln Tyr Ala	Ala Ser Val Phe Leu Gly Trp Ala
	40
Thr Lys Lys Phe Gly Lys Arg Asn	Thr Ile Trp Leu Phe Gly Pro Ala
	45
Thr Thr Gly Lys Thr Asn Ile Ala	Glu Ala Ile Ala His Ala Val Pro
	50
Phe Tyr Gly Cys Val Asn Trp Thr	Asn Glu Asn Phe Pro Phe Asn Asp
	55
Cys Val Asp Lys Met Val Ile Trp	Trp Glu Glu Gly Lys Met Thr Ala
	60
Lys Val Val Glu Ser Ala Lys Ala	Ile Leu Gly Gly Ser Lys Val Arg
	65
Val Asp Gln Lys Cys Lys Ser Ser	Ala Gln Ile Asp Pro Thr Pro Val
	70
Ile Val Thr Ser Asn Thr Asn Met	Cys Ala Val Ala Asp Gly Asn Ser
	75
Thr Thr Phe Glu His Gln Gln Pro	Leu Gln Asp Arg Met Phe Lys Phe
	80
Glu Leu Thr Arg Arg Leu Asp His	Asp Phe Gly Lys Val Thr Lys Gln
	85
225	230

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Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310						315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325				330						335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 323

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 350 428 GCT GCT

&lt;400&gt; 323

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala

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Ser	Asn	Ser	Arg	245	Gln	Ile	Lys	Ala	250	Ala	Leu	Asp	Asn	Ala	255	Gly	Lys
			260	Ser	Thr	Lys	Thr	Ala	265	Pro	Asp	Tyr	Leu	Val	270	Gly	Gln
Ile	Met	Ser	Leu	275				280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290				295						300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
				325					330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro		
			340					345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
				405					410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser		
			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475				480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515				520						525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

&lt;210&gt; 324

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 350 428 GCT GCT

&lt;400&gt; 324

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 325

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 78 54 338 495 GCC GCC GCC

&lt;400&gt; 325

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325				330						335	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345				350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405				410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565				570						575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 326

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 338 495 GCC GCC GCC

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&lt;400&gt; 326

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 327

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 338 495 GCC GCC GCC

&lt;400&gt; 327



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Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala

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				485					490					495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

<210> 328  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 54 338 495 GCC GCC GCC

<400> 328																	
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10					15				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55						60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75					80		
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
				85				90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170					175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
				245					250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			260					265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
305					310												

<210> 329  
 <211> 621  
 <212> PRT

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 350 420 GCT GCC

&lt;400&gt; 329

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

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		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	515					520					525						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
530					535						540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545				550					555						560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565					570						575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		580				585						590					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	595				600						605						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610				615						620						

&lt;210&gt; 330

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 350 420 GCT GCC

&lt;400&gt; 330

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
		20				25							30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
	35	-				40						45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
50				55						60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65			70						75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
		100					105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro		
	115					120					125						
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
130				135					140								
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145			150						155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
	180					185						190					
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195				200						205						
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 331

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 350 420 GCT GCC

&lt;400&gt; 331

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 332

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 350 420 GCT GCC

&lt;400&gt; 332

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55				60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

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<210> 333  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 189 197 518 GCG GCG GCA

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<400> 333
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His

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Leu	Thr	His	180	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195						200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405				410						415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420				425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ala	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys												

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<210> 334
<211> 397
<212> PRT
<213> Artificial Sequence
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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 189 197 518 GCG GCG GCA

&lt;400&gt; 334

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275     280     285
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
 305     310     315     320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
 325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
 340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
 355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385     390     395

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&lt;210&gt; 335

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;223&gt; Mutant rep protein: rep68 189 197 518 GCG GCG GCA

&lt;400&gt; 335

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Ala	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 336

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 189 197 518 GCG GCG GCA

&lt;400&gt; 336

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

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<210> 337  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 468 516 GCC GCG

<400> 337  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

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&lt;210&gt; 338

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 468 516 GCC GCG

&lt;400&gt; 338

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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		195					200				205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Ala	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245						250				255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 339

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 468 516 GCC GCG

&lt;400&gt; 339

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85				90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			



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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370 375 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 450 455 460
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 500 505 510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 515 520 525
Arg Leu Ala Arg Gly His Ser Leu
 530 535

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&lt;210&gt; 340

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 468 516 GCC GCG

&lt;400&gt; 340

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1 5 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20 25 30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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65	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	80
					85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150				155						160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170						175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195						200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Ala	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
				245				250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			260					265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
	275						280					285					
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
305					310												

&lt;210&gt; 341

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant-rep protein: rep78 127 221 350 54 140 GCT  
GCA GCT GCC GCC

&lt;400&gt; 341

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5				10						15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85				90					95				
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
		100						105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Ala	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		

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145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg
	210					215					220			Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val
		340					345					350		Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355				360					365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420					425					430		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440				445			Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490						Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500				505						510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515				520						525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
545					550					555				Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			565						570					Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
		580					585					590		Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	595						600					605		Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
	610					615						620		

&lt;210&gt; 342

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<211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 127 221 350 54 140 GCT  
 GCA GCT GCC GCC

<400> 342  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 343

-402-

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 127 221 350 54 140 GCT

GCA GCT GCC GCC

&lt;400&gt; 343

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	1	5	10	15
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	20	25	30	
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	35	40	45	
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	50	55	60	
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	65	70	75	80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	85	90	95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	100	105	110	
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Ala	Leu	115	120	125	
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly	130	135	140	
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	145	150	155	160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	165	170	175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	180	185	190	
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	195	200	205	
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr	210	215	220	
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	225	230	235	240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	245	250	255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Leu	Asp	Asn	Ala	Gly	Lys		260	265	270	
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	275	280	285	
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	290	295	300	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	305	310	315	320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	325	330	335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro	340	345	350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	355	360	365	
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	370	375	380	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Ser	Lys	Val	Arg		385	390	395	400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	405	410	415	

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
              420              425              430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
              435              440              445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
              450              455              460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
              465              470              475              480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485              490              495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
              500              505              510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
              515              520              525
Arg Leu Ala Arg Gly His Ser Leu
              530              535

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&lt;210&gt; 344

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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<223> Mutant rep protein rep40 127 221 350 54 140 GCT
      GCA GCT GCC GCC

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&lt;400&gt; 344

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1              5              10              15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
              20              25              30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
              35              40              45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
              50              55              60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
              65              70              75              80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
              85              90              95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              100              105              110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
              115              120              125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
              130              135              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
              145              150              155              160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
              165              170              175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
              180              185              190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
              195              200              205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
              210              215              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
              225              230              235              240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
              245              250              255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              260              265              270

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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
                   305                  310

&lt;210&gt; 345

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 221 285 GCA GCG

&lt;400&gt; 345

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
   1                  5                  10                  15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                  25                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                  40                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
                   50                  55                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
   65                  70                  75                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                  90                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                  105                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
                   115                  120                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
                   130                  135                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
   145                  150                  155                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                  170                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                  185                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                  200                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr  
                   210                  215                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   225                  230                  235                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   245                  250                  255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   260                  265                  270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln  
                   275                  280                  285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   290                  295                  300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
   305                  310                  315                  320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   325                  330                  335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   340                  345                  350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp



		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485				490						495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

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<220>
<223> Mutant rep protein: rep52 221 285 GCA GCG
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<400>	346															
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Ala	Gly	Gln	Gln	
50					55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
130						135					140					

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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 347

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 285 GCA GCG

&lt;400&gt; 347

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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145	Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
					165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			245					250						255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Ala	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			325					330						335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		340						345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			405					410						415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		420					425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			485					490						495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		500					505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515				520						525				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu									
	530					535										

&lt;210&gt; 348

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 285 GCA GCG

&lt;400&gt; 348

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	

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Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Ala	Gly	Gln	Gln	
	50				55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85					90						95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
		180						185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	290					295					300					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu									
305					310											

&lt;210&gt; 349

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 23 495 GCT GCC

&lt;400&gt; 349

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1			5						10					15		
Glu	His	Leu	Pro	Gly	Ile	Ala	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
		20						25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
			85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	

			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150						155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450														

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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
           595                          600          605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
       610                          615          620

<210> 350  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 23 495 GCT GCC

<400> 350  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
           20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
           35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
           85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
           100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
           115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
           130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
           165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
           180                  185                  190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
           195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
           210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
           245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
           260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
           275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           290                  295                  300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
   305                  310                  315                  320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
           325                  330                  335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
           340                  345                  350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
           355                  360                  365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

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370                      375                      380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385                      390                      395

<210> 351  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 23 495 GCT GCC

<400> 351  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1                      5                      10                      15  
 Glu His Leu Pro Gly Ile Ala Asp Ser Phe Val Asn Trp Val Ala Glu  
 20                      25                      30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35                      40                      45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50                      55                      60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65                      70                      75                      80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85                      90                      95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100                      105  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115                      120  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130                      135                      140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145                      150                      155                      160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165                      170                      175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180                      185                      190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195                      200                      205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210                      215                      220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225                      230                      235                      240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245                      250                      255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260                      265                      270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275                      280                      285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290                      295                      300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305                      310                      315                      320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325                      330                      335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340                      345                      350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355                      360                      365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370                      375                      380



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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 352

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 23 495 GCT GCC

&lt;400&gt; 352

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val

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				245					250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			260					265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
305					310												

&lt;210&gt; 353

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep78 20 54 420 495 GCC GCC  
GCC GCC

&lt;400&gt; 353

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5				10						15			
Glu	His	Leu	Ala	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
			85					90						95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
		115				120						125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165					170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
			180					185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195				200						205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245					250						255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265					270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		

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				325					330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
			340					345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		420						425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500					505						510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	515					520						525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565					570						575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		580					585						590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	595					600						605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610				615						620						

&lt;210&gt; 354

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep52 20 54 420 495 GCC GCC  
GCC GCC

&lt;400&gt; 354

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10					15				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
		20				25						30					
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
	35					40					45						
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70				75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		

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			100					105				110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
	195						200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	290					295					300					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
305					310					315					320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
				325					330					335		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
			340					345					350			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
		355					360					365				
Ile	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	370				375					380						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
385					390					395						

&lt;210&gt; 355

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep68 20 54 420 495 GCC GCC  
GCC GCC

&lt;400&gt; 355

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1			5					10					15			
Glu	His	Leu	Ala	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
		20						25				30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50				55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
			85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	

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Arg	Glu	Lys	100	Leu	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	110	Glu	Pro	Thr	Leu
		115						120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
	130					135					140							
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
				165					170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185						190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325					330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
				405					410					415				
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala			
				485					490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 356

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

<223> Mutant rep protein: rep40 20 54 420 495 GCC GCC  
GCC GCC

&lt;400&gt; 356

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 357

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep78 412 612 GCG GCG

&lt;400&gt; 357

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			

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Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu



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530		535		540												
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555						560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570						575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Ala	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

&lt;210&gt; 358

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 412 612 GCC GCG

&lt;400&gt; 358

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245				250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320

Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Ala	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

<220>  
<223> Mutant rep protein: rep68 412 612 GCC GCG

<div><div>&lt;400&gt;</div><div>359</div></div>	Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1	Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
				20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	

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Thr	Thr	Gly	Lys	325	Thr	Asn	Ile	Ala	Glu	330	Ala	Ile	Ala	His	Thr	335	Val	Pro
			340						345						350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475				480				
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500				505						510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 360

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 412 612 GCC GCG

&lt;400&gt; 360

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
			180					185					190		

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 361

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 412 GCG GCC

&lt;400&gt; 361

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

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		275					280				285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615									

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<220>
<223> Mutant rep protein: rep52 197 412 GCG GCC
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<400> 362
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10         15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50          55          60

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305     310     315     320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385     390     395

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&lt;210&gt; 363

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 412 GCG GCC

&lt;400&gt; 363

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

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65					70					75				80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
				85					90					95
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
			100					105					110	
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
		115					120					125		
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
	130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145					150				155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
			165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
		180						185				190		His
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
	195					200					205			Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
	210					215					220			Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
			245						250				255	Ala
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
		260					265					270		Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
	275					280					285			Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290				295					300				Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			325					330					335	Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355					360					365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370				375					380				Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro
			405					410					415	Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420					425					430		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	435						440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490					495	Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		500					505					510		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520						525		Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 364



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<211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 197 412 GCG GCC

<400> 364  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 365  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 412 495 511 GCC GCC GCA

<400> 365  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

			20					25				30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370														

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Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 366

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 412 495 511 GCC GCC GCA

&lt;400&gt; 366

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165				170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245				250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp

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290	295	300
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly	Met Asn Leu Met Leu
305	310	315
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys
325	330	335
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu
340	345	350
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr
355	360	365
Ile His His Ile Met Gly	Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp
370	375	380
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe	Glu Gln
385	390	395

&lt;210&gt; 367

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 412 495 511 GCC GCC GCA

&lt;400&gt; 367

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	1	5	10	15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	20	25	30	
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	35	40	45	
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	50	55	60	
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	65	70	75	80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	85	90	95	
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	100	105	110	
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	115	120	125	
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	130	135	140	
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	145	150	155	160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu	165	170	175	
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His	180	185	190	
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn	195	200	205	
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr	210	215	220	
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	225	230	235	240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	245	250	255	
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	260	265	270	
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	275	280	285	
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	290	295	300	

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
          530          535

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<210> 368  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 412 495 511 GCC GCC GCA

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<400> 368
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 369

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 98 422 GCC GCC

&lt;400&gt; 369

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85				90						95	
Thr	Ala	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610      615      620

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&lt;210&gt; 370

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 98 422 GCC GCC

&lt;400&gt; 370

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180				185						190		
Ile	Val	Thr	Ser	Asn	Ala	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340				345						350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390										

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<220>
<223> Mutant rep protein: rep68 98 422 GCC GCC
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<400> 371
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  35          40          45

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Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Ala	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys</												

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530

535

<210> 372  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 98 422 GCC GCC

<400> 372  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 373  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 17 127 189 GCG GCT GCG

<400> 373

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

Pro	Ser	Asp	Ala	485	Ile	Ser	Glu	Pro	490	Lys	Arg	Val	Arg	Glu	495	Ser	Val
			500					505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
				565					570						575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

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<220>
<223> Mutant rep protein: rep68 17 127 189 GCG GCT GCG
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<400>	374															
Thr 1	Ala	Gly	Phe	Tyr 5	Glu	Ile	Val	Ile	Lys 10	Val	Pro	Ser	Asp	Leu 15	Asp	
Ala	His	Leu	Pro 20	Gly	Ile	Ser	Asp	Ser 25	Phe	Val	Asn	Trp	Val 30	Ala	Glu	
Lys	Glu	Trp 35	Glu	Leu	Pro	Pro	Asp 40	Ser	Asp	Met	Asp	Leu 45	Asn	Leu	Ile	
Glu	Gln 50	Ala	Pro	Leu	Thr	Val 55	Ala	Glu	Lys	Leu	Gln 60	Arg	Asp	Phe	Leu	
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val 80	
Gln	Phe	Glu	Lys 85	Gly	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu	
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile	
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu	Pro 125	Ala	Leu	
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly	
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160	
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu	
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Ala	Ala 190	Gln	His	
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn	
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr	
Met 225	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240	
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala	
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys	

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Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325				330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 375

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 20 54 495 GCC GCC GCC

&lt;400&gt; 375

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Ala	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly

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130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
	210	215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
	290	295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620



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<210> 376  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 20 54 495 GCC GCC GCC

<400> 376  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 377

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<211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 20 54 495 GCC GCC GCC

<400> 377  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			485					490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500						505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	515					520						525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

&lt;210&gt; 378

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 20 54 495 GCC GCC GCC

&lt;400&gt; 378

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
		20					25						30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
	35					40					45						
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
50					55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70					75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
		100					105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
	115					120						125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130				135					140							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145				150					155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
	180						185						190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195					200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
	260					265							270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
	275					280						285					

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 379  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 259 54 GCG GCC

<400> 379  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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370	375	380
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
385	390	395
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile	Asp Pro Thr Pro Val
405	410	415
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ser
420	425	430
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe
435	440	445
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln
450	455	460
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val
465	470	475
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala	Lys Lys Arg Pro Ala
485	490	495
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val
500	505	510
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp
515	520	525
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly	Met Asn Leu Met Leu
530	535	540
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys
545	550	555
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu
565	570	575
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr
580	585	590
Ile His His Ile Met Gly	Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp
595	600	605
Leu Val Asn Val Asp Leu	Asp Cys Ile Phe Glu	Gln 620
610	615	

&lt;210&gt; 380

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 259 54 GCG GCC

&lt;400&gt; 380

Met Glu Leu Val Gly Trp	Leu Val Asp Lys Gly	Ile Thr Ser Glu Lys
1	5	10
Gln Trp Ile Gln Glu Asp	Gln Ala Ser Tyr Ile	Ser Phe Asn Ala Ala
20	25	30
Ser Asn Ala Arg Ser Gln	Ile Lys Ala Ala Leu	Asp Asn Ala Gly Lys
35	40	45
Ile Met Ser Leu Thr Lys	Thr Ala Pro Asp Tyr	Leu Val Gly Gln Gln
50	55	60
Pro Val Glu Asp Ile Ser	Ser Asn Arg Ile Tyr	Lys Ile Leu Glu Leu
65	70	75
Asn Gly Tyr Asp Pro Gln	Tyr Ala Ala Ser Val	Phe Leu Gly Trp Ala
85	90	95
Thr Lys Lys Phe Gly Lys	Arg Asn Thr Ile Trp	Leu Phe Gly Pro Ala
100	105	110
Thr Thr Gly Lys Thr Asn	Ile Ala Glu Ala Ile	Ala His Thr Val Pro
115	120	125
Phe Tyr Gly Cys Val Asn	Trp Thr Asn Glu Asn	Phe Pro Phe Asn Asp
130	135	140
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu	Gly Lys Met Thr Ala
145	150	155
		160

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 381

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant\_rep protein: rep68 259 54 GCG GCC

&lt;400&gt; 381

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225				230						235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			245					250						255		
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305				310						315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			325					330						335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		340						345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385				390						395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			405					410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		420						425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465				470						475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			485					490						495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		500														

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<400> 382
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20          25          30

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Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 383

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 335 399 GCT GCG

&lt;400&gt; 383

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu

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Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
130						135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
210						215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
290						295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
370						375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Ala	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
450						455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
530						535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600						605		

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

<210> 384  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 335 399 GCT GCG

<400> 384  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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385

390

395

&lt;210&gt; 385

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 335 399 GCT GCG

&lt;400&gt; 385

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Ala	Arg
385					390					395					400

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 386

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 335 399 GCT GCG

&lt;400&gt; 386

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Ala	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala

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			260					265				270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 387

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 221 432 GCA GCA

&lt;400&gt; 387

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75						80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
	115						120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150				155						160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
	195					200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250						255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   355                  360                  365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
                   370                  375                  380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   385                  390                  395                  400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                   405                  410                  415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala  
                   420                  425                  430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   435                  440                  445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
                   450                  455                  460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   465                  470                  475                  480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   485                  490                  495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   500                  505                  510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   515                  520                  525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
                   530                  535                  540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
                   545                  550                  555                  560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                   565                  570                  575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                   580                  585                  590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
                   595                  600                  605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
                   610                  615                  620

&lt;210&gt; 388

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 221 432 GCA GCA

&lt;400&gt; 388

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp



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130	135	140
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu	Gly Lys Met Thr Ala
145	150	155
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
165	170	175
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile	Asp Pro Thr Pro Val
180	185	190
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ala
195	200	205
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe
210	215	220
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln
225	230	235
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val
245	250	255
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala	Lys Lys Arg Pro Ala
260	265	270
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val
275	280	285
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp
290	295	300
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly	Met Asn Leu Met Leu
305	310	315
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys
325	330	335
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu
340	345	350
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr
355	360	365
Ile His His Ile Met Gly	Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp
370	375	380
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe	Glu Gln
385	390	395

&lt;210&gt; 389

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 432 GCA GCA

&lt;400&gt; 389

Thr Ala Gly Phe Tyr Glu Ile Val Ile	Lys Val Pro Ser Asp Leu Asp
1	10
Glu His Leu Pro Gly Ile Ser Asp Ser	Phe Val Asn Trp Val Ala Glu
20	25
Lys Glu Trp Glu Leu Pro Pro Asp Ser	Asp Met Asp Leu Asn Leu Ile
35	40
Glu Gln Ala Pro Leu Thr Val Ala Glu	Lys Leu Gln Arg Asp Phe Leu
50	55
Thr Glu Trp Arg Arg Val Ser Lys Ala	Pro Glu Ala Leu Phe Phe Val
65	70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe	His Met His Val Leu Val Glu
85	90
Thr Thr Gly Val Lys Ser Met Val Leu	Gly Arg Phe Leu Ser Gln Ile
100	105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr	Arg Gly Ile Glu Pro Thr Leu
115	120
Pro Asn Trp Phe Ala Val Thr Lys Thr	Arg Asn Gly Ala Gly Gly Gly
130	135
	140

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Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
	210				215						220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275				280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290				295						300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345				350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355				360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370				375						380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ala
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435				440						445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450				455						460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470						475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		500					505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515				520						525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530				535										

&lt;210&gt; 390

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 432 GCA GCA

&lt;400&gt; 390

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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1				5				10					15				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75				80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
				85					90					95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155				160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170					175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ala		
		195					200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235				240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
				245					250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			260					265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
305					310												

&lt;210&gt; 391

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 259 516 GCG GCG

&lt;400&gt; 391

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5					10				15				
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25				30					
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75				80			
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			

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Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr

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			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 392

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 259 516 GCG GCG

&lt;400&gt; 392

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5					10					15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
		20						25					30				
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55						60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70					75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100				105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115				120						125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130				135				140								
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145				150					155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180					185						190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230				235					240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260					265						270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275				280						285					
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290				295						300						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
305				310					315					320			
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
			325					330					335				
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
		340				345						350					
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
	355					360						365					

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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 393  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 259 516 GCG GCG

<400> 393  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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370	375	380
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
385	390	395
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile Asp	Pro Thr Pro Val
405	410	415
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val Ile	Asp Gly Asn Ser
420	425	430
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp Arg	Met Phe Lys Phe
435	440	445
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly Lys	Val Thr Lys Gln
450	455	460
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp His	Val Val Glu Val
465	470	475
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala Lys	Lys Arg Pro Ala
485	490	495
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg Val	Arg Glu Ser Val
500	505	510
Ala Gln Pro Ala Thr Ser	Asp Ala Glu Ala Ser Ile	Asn Tyr Ala Asp
515	520	525
Arg Leu Ala Arg Gly His	Ser Leu	
530	535	

&lt;210&gt; 394

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 259 516 GCG GCG

&lt;400&gt; 394

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	1	5	10	15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	20	25	30	
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	35	40	45	
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	50	55	60	
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	65	70	75	80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	85	90	95	
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	100	105	110	
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	115	120	125	
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	130	135	140	
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	145	150	155	160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	165	170	175	
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val	180	185	190	
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	195	200	205	
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	210	215	220	
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	225	230	235	240



Glu	Val	Lys	Asp	Phe 245	Phe	Arg	Trp	Ala	Lys 250	Asp	His	Val	Val	Glu 255	Val
Glu	His	Glu	Phe	Tyr 260	Val	Lys	Lys	Gly 265	Gly	Ala	Lys	Lys	Arg	Pro	Ala
Pro	Ser	Asp 275	Ala	Asp	Ile	Ser	Glu 280	Pro	Lys	Arg	Val	Arg 285	Glu	Ser	Val
Ala	Gln 290	Pro	Ala	Thr	Ser	Asp 295	Ala	Glu	Ala	Ser	Ile 300	Asn	Tyr	Ala	Asp
Arg 305	Leu	Ala	Arg	Gly	His 310	Ser	Leu								

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<210> 395
<211> 621
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mutant rep protein: rep78 495 516 GCC GCG
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<400>	395															
Thr 1	Ala	Gly	Phe	Tyr 5	Glu	Ile	Val	Ile	Lys 10	Val	Pro	Ser	Asp	Leu 15	Asp	
Glu	His	Leu	Pro	Gly 20	Ile	Ser	Asp	Ser 25	Phe	Val	Asn	Trp	Val 30	Ala	Glu	
Lys	Glu	Trp 35	Glu	Leu	Pro	Pro	Asp 40	Ser	Asp	Met	Asp	Leu 45	Asn	Leu	Ile	
Glu	Gln 50	Ala	Pro	Leu	Thr	Val 55	Ala	Glu	Lys	Leu	Gln 60	Arg	Asp	Phe	Leu	
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80	
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu	
Thr	Thr	Gly 100	Val	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile	
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile	Tyr 120	Arg	Gly	Ile	Glu	Pro 125	Thr	Leu	
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr 135	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly	
Asn 145	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160	
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu	
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His	
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln	Glu 200	Gln	Asn	Lys	Glu	Asn 205	Gln	Asn	
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr	
Met 225	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys 240	
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala	
Ser	Asn	Ser	Arg	Ser 260	Gln	Ile	Lys	Ala	Ala 265	Leu	Asp	Asn	Ala 270	Gly	Lys	
Ile	Met	Ser	Leu	Thr 275	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly 285	Gln	Gln	
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu	
Asn 305	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala 320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	

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Thr	Thr	Gly	Lys	325	Thr	Asn	Ile	Ala	Glu	330	Ala	Ile	Ala	His	Thr	335	Val	Pro
			340							345						350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
		370				375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
				405					410						415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425						430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
	515						520					525						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu			
	530					535					540							
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys			
545					550					555					560			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu			
			565					570						575				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr			
			580					585					590					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
	595					600					605							
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln						
	610					615					620							

&lt;210&gt; 396

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 495 516 GCC GCG

&lt;400&gt; 396

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 397

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 516 GCC GCG

&lt;400&gt; 397

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
130						135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
210						215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
290						295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520						525		
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
530						535									

&lt;210&gt; 398

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 495 516 GCC GCG

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<400> 398  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 399

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence .

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 414 14 GCT GCC

&lt;400&gt; 399

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Ala Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80

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Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275				280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355				360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Ala	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 565 570 575  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 580 585 590  
 Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln  
 595 600 605  
 610 615 620

<210> 400  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 414 14 GCT GCC

<400> 400  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350



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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 401

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 414 14 GCT GCC

&lt;400&gt; 401

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Ala Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 402

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 414 14 GCT GCC

&lt;400&gt; 402

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 403

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 74 402 495 GCG GCC GCC

&lt;400&gt; 403

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Ala	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500				505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515				520						525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580				585						590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 404

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 74 402 495 GCG GCC GCC

&lt;400&gt; 404

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35				40						45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55				60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 405

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 74 402 495 GCG GCC GCC

&lt;400&gt; 405

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

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Arg	Glu	Lys	100	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	110	Glu	Pro	Thr	Leu
		115	..				120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	135	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130											140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	150	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					155						155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	170	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
			165												175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	185	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180												190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	200	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195											205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	215	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210											220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	230	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					235						235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	245	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
											250				255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	260	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			265											270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	280	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275												285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	295	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290											300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	310	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					315						315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	325	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
											330				335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	340	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			345											350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	355	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355											365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	370	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375						380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	385	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
					390						395					400	
Val	Ala	Gln	Lys	Cys	Lys	Ser	Ser	405	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
											410				415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	420	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			425											430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	435	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		440												445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	445	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455						460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	465	Ala	Lys	Asp	His	Val	Val	Glu	Val	
					470						475				480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	485	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
											490				495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	500	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			505											510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	515	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
													525				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu	530									
								535									

&lt;210&gt; 406

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 74 402 495 GCG GCC GCC

&lt;400&gt; 406

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 407

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 228 462 497 GCC GCC GCC

&lt;400&gt; 407

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

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50	55	60													
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115				120						125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Ala	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				

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Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 408

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 228 462 497 GCC GCC GCC

&lt;400&gt; 408

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

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				325					330					335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			340					345					350				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		355					360					365					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	370					375					380						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
385					390					395							

&lt;210&gt; 409

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 228 462 497 GCC GCC GCC

&lt;400&gt; 409

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1			5					10					15				
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
		20					25					30					
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55				60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
			85						90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
		100						105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165						170					175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
		180						185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245						250					255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		260						265					270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			325						330					335			

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 410

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 228 462 497 GCC GCC GCC

&lt;400&gt; 410

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

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<210> 411
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 290 338 GCG GCC

```

```

<400> 411
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285

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```

Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290                295                300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                310                315                320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                330                335
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340                345                350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355                360                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370                375                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                390                395                400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                470                475                480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                515                520                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530                535                540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545                550                555                560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565                570                575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                580                585                590
Ile His His Fle Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595                600                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610                615                620

```

&lt;210&gt; 412

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 290 338 GCG GCC

&lt;400&gt; 412

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1                5                10                15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                20                25                30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35                40                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50                55                60
Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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65					70					75				80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
				85					90					95
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			100					105					110	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
		115					120				125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	130					135					140			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
145					150					155				160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
				165					170					175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
		180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
	195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
225					230					235				240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
			245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
		260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
	275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
305				310						315				320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
			325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
		340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
	355				360					365				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	370				375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
385					390					395				

&lt;210&gt; 413

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 290 338 GCG GCC

&lt;400&gt; 413

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
	35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55						60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75					80	



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Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Ala	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

<210> 414  
 <211> 312

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 290 338 GCG GCC

&lt;400&gt; 414

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100     105     110
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290     295     300
Arg Leu Ala Arg Gly His Ser Leu
 305     310

```

&lt;210&gt; 415

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 140 511 GCC GCA

&lt;400&gt; 415

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30

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Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp

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		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580				585						590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 416

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 140 511 GCC GCA

&lt;400&gt; 416

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70				75						80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100				105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115				120						125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145				150					155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230				235					240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val		
		275				280						285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 417  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 140 511 GCC GCA

<400> 417  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360				365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405						410					415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420						425					430	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455				460				Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490						495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala
		500					505					510		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520						525		Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 418

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 140 511 GCC GCA

&lt;400&gt; 418

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40				45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85				90						95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135				140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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<210> 419  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 86 378 GCG GCG

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<400> 419
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```



			260					265				270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355						360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Ala	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615</									

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<220>
<223> Mutant rep protein: rep52 86 378 GCG GCG
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<400> 420
Met  Glu  Leu  Val  Gly  Trp  Leu  Val  Asp  Lys  Gly  Ile  Thr  Ser  Glu  Lys
 1      5      10      15
Gln  Trp  Ile  Gln  Glu  Asp  Gln  Ala  Ser  Tyr  Ile  Ser  Phe  Asn  Ala  Ala
 20      25      30
Ser  Asn  Ser  Arg  Ser  Gln  Ile  Lys  Ala  Ala  Leu  Asp  Asn  Ala  Gly  Lys
 35      40      45

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Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Ala	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215						220			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 421

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 68 86 378 GCG GCG

&lt;400&gt; 421

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu



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<210> 422  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 86 378 GCG GCG

<400> 422  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 423  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 54 86 GCC GCG

<400> 423  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
		50				55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Ala	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130				135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290				295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val

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			500					505				510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

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<210> 424
<211> 536
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mutant rep protein: rep68 54 86 GCC GCG
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<400> 424																
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1				5					10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
			20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
50						55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Ala	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 425

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 86 GCC GCG

&lt;400&gt; 425

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
	210					215					220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
	305				310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360					365		
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
	385				390					395				400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420					425					430	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
	465				470					475				480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
				485					490					495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
	545				550					555				560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
				565					570					575
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
			580					585					590	
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
		595					600					605		
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
	610					615					620			

&lt;210&gt; 426

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<211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 54 86 GCC GCG

<400> 426  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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			420					425				430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 427

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 214 495 140 GCG GCC GCC

&lt;400&gt; 427

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Ala	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

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&lt;210&gt; 428

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 214 495 140 GCG GCC GCC

&lt;400&gt; 428

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120				125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130				135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155						160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
	195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235						240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245				250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
	275						280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290				295						300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
	355						360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370				375						380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 429

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 214 495 140 GCG GCC GCC

&lt;400&gt; 429

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80

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Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150						155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Ala	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250						255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470						475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		500					505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 430

&lt;211&gt; 312

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 214 495 140 GCG GCC GCC

&lt;400&gt; 430

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

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&lt;210&gt; 431

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 495 511 GCC GCA

&lt;400&gt; 431

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30

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Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260				265						270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp

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		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580				585						590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	595					600						605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 432

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 495 511 GCC GCA

&lt;400&gt; 432

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70				75						80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100				105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115				120						125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130				135					140							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145				150					155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180				185						190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230				235					240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
		260				265						270					
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val		
		275				280						285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305          310          315          320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385          390          395

```

&lt;210&gt; 433

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 511 GCC GCA

&lt;400&gt; 433

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75     80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130    135    140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145    150    155    160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165    170    175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180    185    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195    200    205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210    215    220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225    230    235    240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245    250    255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260    265    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275    280    285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290    295    300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
          530          535

```

<210> 434  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 495 511 GCC GCA

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<400> 434
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          165          170          175

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 435

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 495 54 GCC GCC

&lt;400&gt; 435

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65				70						75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215						220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys

			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600		</							

```
<220>
<223> Mutant rep protein: rep52 495 54 GCC GCC
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```
<400> 436
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
```

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Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75						80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
			260					265				270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 437

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 54 GCC GCC

&lt;400&gt; 437

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu



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50	55	60
Thr Glu Trp Arg Arg Val	Ser Lys Ala Pro Glu	Ala Leu Phe Phe Val
65	70	75
Gln Phe Glu Lys Gly Glu	Ser Tyr Phe His Met	His Val Leu Val Glu
85	90	95
Thr Thr Gly Val Lys Ser	Met Val Leu Gly Arg	Phe Leu Ser Gln Ile
100	105	110
Arg Glu Lys Leu Ile Gln	Arg Ile Tyr Arg Gly	Ile Glu Pro Thr Leu
115	120	125
Pro Asn Trp Phe Ala Val	Thr Lys Thr Arg Asn	Gly Ala Gly Gly Gly
130	135	140
Asn Lys Val Val Asp Glu	Cys Tyr Ile Pro Asn	Tyr Leu Leu Pro Lys
145	150	155
Thr Gln Pro Glu Leu Gln	Trp Ala Trp Thr Asn	Met Glu Gln Tyr Leu
165	170	175
Ser Ala Cys Leu Asn Leu	Thr Glu Arg Lys Arg	Leu Val Ala Gln His
180	185	190
Leu Thr His Val Ser Gln	Thr Gln Glu Gln Asn	Lys Glu Asn Gln Asn
195	200	205
Pro Asn Ser Asp Ala Pro	Val Ile Arg Ser Lys	Thr Ser Ala Arg Tyr
210	215	220
Met Glu Leu Val Gly Trp	Leu Val Asp Lys Gly	Ile Thr Ser Glu Lys
225	230	235
Gln Trp Ile Gln Glu Asp	Gln Ala Ser Tyr Ile	Ser Phe Asn Ala Ala
245	250	255
Ser Asn Ser Arg Ser Gln	Ile Lys Ala Leu Asp	Asn Ala Gly Lys
260	265	270
Ile Met Ser Leu Thr Lys	Thr Ala Pro Asp Tyr	Leu Val Gly Gln Gln
275	280	285
Pro Val Glu Asp Ile Ser	Ser Asn Arg Ile Tyr	Lys Ile Leu Glu Leu
290	295	300
Asn Gly Tyr Asp Pro Gln	Tyr Ala Ala Ser Val	Phe Leu Gly Trp Ala
305	310	315
Thr Lys Lys Phe Gly Lys	Arg Asn Thr Ile Trp	Leu Phe Gly Pro Ala
325	330	335
Thr Thr Gly Lys Thr Asn	Ile Ala Glu Ala Ile	Ala His Thr Val Pro
340	345	350
Phe Tyr Gly Cys Val Asn	Trp Thr Asn Glu Asn	Phe Pro Phe Asn Asp
355	360	365
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu	Gly Lys Met Thr Ala
370	375	380
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
385	390	395
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile	Asp Pro Thr Pro Val
405	410	415
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ser
420	425	430
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe
435	440	445
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln
450	455	460
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val
465	470	475
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala	Lys Lys Arg Ala Ala
485	490	495
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val
500	505	510
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp
515	520	525
Arg Leu Ala Arg Gly His	Ser Leu	
530	535	

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<210> 438  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 495 54 GCC GCC

<400> 438  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 439  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 197 495 GCG GCC

<400> 439  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345						350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val

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			500					505				510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
			565						570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
		580					585						590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
	595					600						605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

&lt;210&gt; 440

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 495 GCG GCC

&lt;400&gt; 440

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5				10						15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
		20					25						30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
	35					40						45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
	50				55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85					90						95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
	115						120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
			165					170						175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
		180						185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
	195					200						205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
			245					250						255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
		260						265				270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
	275						280					285				

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Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 441

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 495 GCG GCC

&lt;400&gt; 441

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40				45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85				90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185						190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu

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290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Leu Ala Arg Gly His Ser Leu		525
530	535	

&lt;210&gt; 442

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 495 GCG GCC

&lt;400&gt; 442

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
	85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
	100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	
	115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	
	130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	
145	150
	155
	160

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 443

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 261 20 GCC GCC

&lt;400&gt; 443

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala



				245					250					255		
Ser	Asn	Ser	Arg	Ala	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475				480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585								

```
<400> 444
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20          25          30
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Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
   35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
  260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
  325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
  340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
  355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  385      390      395

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&lt;210&gt; 445

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 261 20 GCC GCC

&lt;400&gt; 445

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

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		35					40				45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ala	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			

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Arg Leu Ala Arg Gly His Ser Leu  
530 535

<210> 446  
<211> 312  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep40 261 20 GCC GCC

<400> 446  
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
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Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
35 40 45  
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
50 55 60  
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
65 70 75 80  
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
85 90 95  
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
100 105 110  
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
115 120 125  
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
130 135 140  
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
145 150 155 160  
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
165 170 175  
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
180 185 190  
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
195 200 205  
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
210 215 220  
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
225 230 235 240  
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
245 250 255  
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
260 265 270  
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
275 280 285  
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
290 295 300  
Arg Leu Ala Arg Gly His Ser Leu  
305 310

<210> 447  
<211> 621  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep78 54 20 GCC GCC

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<400> 447

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
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Glu	His	Leu	Ala	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 448

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 20 GCC GCC

&lt;400&gt; 448

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
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 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355						360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
370						375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
450						455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
530						535									

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<220>
<223> Mutant rep protein: rep78 197 420 GCG GCC
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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			



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Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
130						135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170						175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250						255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275				280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330						335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410						415
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490						495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			

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610 615 620

<210> 450  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 197 420 GCG GCC

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 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

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<210> 451  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220> .  
 <223> Mutant rep protein: rep68 197 420 GCG GCC

<400> 451  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

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Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
              420              425              430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
              435              440              445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
              450              455              460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465              470              475              480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485              490              495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
              500              505              510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
              515              520              525
Arg Leu Ala Arg Gly His Ser Leu
              530              535

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<210> 452
<211> 312
<212> PRT
<213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep40 197 420 GCG GCC

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<400> 452
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20     25     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35     40     45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50     55     60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65     70     75     80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85     90     95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100    105    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115    120    125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130    135    140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145    150    155    160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165    170    175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180    185    190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195    200    205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210    215    220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225    230    235    240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245    250    255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260    265    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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	275		280		285										
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 453

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 338 495 GCC GCC GCC

&lt;400&gt; 453

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
	195						200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215						220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355						360					365			

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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 454

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 338 495 GCC GCC GCC

&lt;400&gt; 454

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215				220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235						240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325					330						335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 455

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 338 495 GCC GCC GCC

&lt;400&gt; 455

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160



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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 456

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 54 338 495 GCC GCC GCC

&lt;400&gt; 456

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75					80		
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
				85					90					95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105						110			
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
	115						120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150				155						160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170					175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195					200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230				235						240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
				245					250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			260					265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
305					310												

&lt;210&gt; 457

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 427 GCG GCG

&lt;400&gt; 457

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1			5					10						15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70				75						80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				

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Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Ala	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
						455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp

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595  
 Leu Val Asn Val Asp Leu Asp 600  
 610 615 Cys Ile Phe Glu 605  
 620 Gln

<210> 458  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 197 427 GCG GCG

<400> 458  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 459

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 427 GCG GCG

&lt;400&gt; 459

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Ala	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440				445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 460

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 427 GCG GCG

&lt;400&gt; 460

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130				135				140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Ala	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245				250						255	

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 461  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 54 228 370 387 GCC GCC  
 GCC GCG

<400> 461  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335



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Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Ala	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Ala	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Ser	Lys	Val	Arg	
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 462

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep52 54 228 370 387 GCC GCC  
GCC GCG

&lt;400&gt; 462

Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

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Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Ala	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Ala	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
	195					200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260					265						270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340						345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 463

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep68 54 228 370 387 GCC GCC  
GCC GCG

&lt;400&gt; 463

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		

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Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Ala	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Ala	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500				505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 464

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-541-

<223> Mutant rep protein: rep40 54 228 370 387 GCC GCC  
GCC GCG

<400> 464

Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70						75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Ala	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150						155				160	
Lys	Val	Ala	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275				280						285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

<210> 465

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 221 289 GCA GCC

<400> 465

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35				40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu

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50	55	60															
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
			115				120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
				165				170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
			180				185						190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
				245					250					255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265					270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
				325					330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
			340					345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
				405					410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475				480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
				485					490					495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						

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Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580				585						590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595				600						605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615				620					

&lt;210&gt; 466

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 221 289 GCA GCC

&lt;400&gt; 466

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20				25						30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130				135						140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165						170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245						250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290				295						300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310					315					320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys

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				325					330					335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			340					345					350				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		355					360					365					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	370					375					380						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
385					390					395							

&lt;210&gt; 467

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 289 GCA GCC

&lt;400&gt; 467

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5				10						15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55				60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
		100						105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135				140							
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
				165					170					175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
		180						185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
				245					250					255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265						270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280						285				
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
				325					330					335			



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Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	515						520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 468

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 289 GCA GCC

&lt;400&gt; 468

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85						90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165						170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser

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		195					200				205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 469

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 163 GCC GCT

&lt;400&gt; 469

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

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&lt;210&gt; 470

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 163 GCC GCT

&lt;400&gt; 470

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

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65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150					155					160	
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185				190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
	195					200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210				215						220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290				295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355				360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370				375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420				425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435				440						445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450				455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	515					520						525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 471

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&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 341 407 420 GCC GCC GCC

&lt;400&gt; 471

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Ala	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ala	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser

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			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455						460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			485					490						495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		500					505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	515						520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
			565					570						575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
		580					585						590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
	595						600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615				620						

&lt;210&gt; 472

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 341 407 420 GCC GCC GCC

&lt;400&gt; 472

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5				10						15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
		20					25						30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
	35						40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
	50					55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65				70					75						80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85				90							95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100				105						110			
Thr	Thr	Gly	Lys	Ala	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
	115						120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
			165						170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ala	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
		180					185						190			
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
	195						200					205				

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Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 473

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 341 407 420 GCC GCC GCC

&lt;400&gt; 473

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr



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210	215	220
Met Glu Leu Val Gly Trp	Leu Val Asp Lys Gly	Ile Thr Ser Glu Lys
225	230	235
Gln Trp Ile Gln Glu Asp	Gln Ala Ser Tyr Ile	Ser Phe Asn Ala Ala
	245	250
Ser Asn Ser Arg Ser Gln	Ile Lys Ala Leu Asp	Asn Ala Gly Lys
	260	265
Ile Met Ser Leu Thr Lys	Thr Ala Pro Asp Tyr	Leu Val Gly Gln Gln
	275	280
Pro Val Glu Asp Ile Ser	Ser Asn Arg Ile Tyr	Lys Ile Leu Glu Leu
	290	295
Asn Gly Tyr Asp Pro Gln	Tyr Ala Ala Ser Val	Phe Leu Gly Trp Ala
305	310	315
Thr Lys Lys Phe Gly Lys	Arg Asn Thr Ile Trp	Leu Phe Gly Pro Ala
	325	330
Thr Thr Gly Lys Ala Asn	Ile Ala Glu Ala Ile	Ala His Thr Val Pro
	340	345
Phe Tyr Gly Cys Val Asn	Trp Thr Asn Glu Asn	Phe Pro Phe Asn Asp
	355	360
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu	Gly Lys Met Thr Ala
	370	375
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
385	390	395
Val Asp Gln Lys Cys Lys	Ala Ser Ala Gln Ile	Asp Pro Thr Pro Val
	405	410
Ile Val Thr Ala Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ser
	420	425
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe
	435	440
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln
	450	455
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val
465	470	475
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala	Lys Lys Arg Pro Ala
	485	490
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val
	500	505
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp
	515	520
Arg Leu Ala Arg Gly His	Ser Ser Leu	
	530	535

<210> 474  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 341 407 420 GCC GCC GCC

<400> 474
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Leu Ala Arg Gly His Ser Leu
305 310

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&lt;210&gt; 475

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant -rep protein: rep78 54 228 GCC GCC

&lt;400&gt; 475

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225				230						235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305				310						315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385				390						395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465				470						475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500													

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<210> 476
<211> 397
<212> PRT
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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 228 GCC GCC

&lt;400&gt; 476

Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215						220			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
			245						250				255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325						330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340						345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 477

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 228 GCC GCC

&lt;400&gt; 477

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180				185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Ser	Lys	Val	Arg	
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln

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450		455		460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val				
465		470		475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala				
	485		490	
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val				
	500		505	
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp				
	515		520	
Arg Leu Ala Arg Gly His Ser Leu			525	
	530		535	

&lt;210&gt; 478

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 54 228 GCC GCC

&lt;400&gt; 478

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys				
1	5	10	15	
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala				
	20	25	30	
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys				
	35	40	45	
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln				
	50	55	60	
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu				
	65	70	75	80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala				
	85	90	95	
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala				
	100	105	110	
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro				
	115	120	125	
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp				
	130	135	140	
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala				
	145	150	155	160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg				
	165	170	175	
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val				
	180	185	190	
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser				
	195	200	205	
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe				
	210	215	220	
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln				
	225	230	235	240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val				
	245	250	255	
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala				
	260	265	270	
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val				
	275	280	285	
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp				
	290	295	300	
Arg Leu Ala Arg Gly His Ser Leu				
	305	310		

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<210> 479  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 96 125 511 GCA GCG GCA

<400> 479  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Ala  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415



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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

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&lt;210&gt; 480

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 96 125 511 GCA GCG GCA

&lt;400&gt; 480

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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		195					200				205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 481

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 96 125 511 GCA GCG GCA

&lt;400&gt; 481

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Ala
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Ala	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
 210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 482

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 96 125 511 GCA GCG GCA

&lt;400&gt; 482

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245				250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 483

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 163 GCC GCT

&lt;400&gt; 483

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90				95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160

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Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 484

&lt;211&gt; 536

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 163 GCC GCT

&lt;400&gt; 484

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		

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Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 485

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 420 GCG GCC

&lt;400&gt; 485

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu



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290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620

&lt;210&gt; 486

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 420 GCG GCC

&lt;400&gt; 486

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70

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Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			260					265				270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310						315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 487

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 420 GCG GCC

&lt;400&gt; 487

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu

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				85				90					95				
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165					170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
		180					185						190				
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195				200						205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210				215						220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245					250						255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		260					265						270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	275					280						285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290				295						300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			325					330						335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		340					345						350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370				375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		420					425						430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450				455						460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500					505						510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515				520						525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

&lt;210&gt; 488

&lt;211&gt; 312

&lt;212&gt; PRT

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 420 GCG GCC

&lt;400&gt; 488

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 489

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 334 428 499 GCG GCT GCC

&lt;400&gt; 489

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

```

		35					40				45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Ala	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390</										

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Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 490

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 334 428 499 GCG GCT GCC

&lt;400&gt; 490

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85						90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Ala	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
					165				170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Ala	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu

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305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

<210> 491  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 334 428 499 GCG GCT GCC

<400> 491															
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40				45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150				155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	



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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 492

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 334 428 499 GCG GCT GCC

&lt;400&gt; 492

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

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Ile	Val	Thr	180	Ser	Asn	Thr	Asn	Met	185	Cys	Ala	Val	Ala	Asp	190	Gly	Asn	Ser
Thr	Thr	195	Phe	Glu	His	Gln	Gln	Pro	200	Leu	Gln	Asp	Arg	Met	205	Phe	Lys	Phe
Glu	Leu	210	Thr	Arg	Arg	Leu	Asp	His	215	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225						230						235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
Pro	Ser	Ala	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
305						310												

&lt;210&gt; 493

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 414 GCG GCT

&lt;400&gt; 493

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130				135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610      615      620

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&lt;210&gt; 494

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 414 GCG GCT

&lt;400&gt; 494

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

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50	55	60
Pro Val Glu Asp Ile Ser	Ser Asn Arg Ile Tyr	Lys Ile Leu Glu Leu
65	70	75
Asn Gly Tyr Asp Pro Gln	Tyr Ala Ala Ser Val	Phe Leu Gly Trp Ala
85	90	95
Thr Lys Lys Phe Gly Lys	Arg Asn Thr Ile Trp	Leu Phe Gly Pro Ala
100	105	110
Thr Thr Gly Lys Thr Asn	Ile Ala Glu Ala Ile	Ala His Thr Val Pro
115	120	125
Phe Tyr Gly Cys Val Asn	Trp Thr Asn Glu Asn	Phe Pro Phe Asn Asp
130	135	140
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu	Gly Lys Met Thr Ala
145	150	155
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg
165	170	175
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile	Asp Pro Ala Pro Val
180	185	190
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ser
195	200	205
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe
210	215	220
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln
225	230	235
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val
245	250	255
Glu His Glu Phe Tyr Val	Lys Lys Gly Ala Lys	Lys Arg Pro Ala
260	265	270
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val
275	280	285
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp
290	295	300
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly	Met Asn Leu Met Leu
305	310	315
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys
325	330	335
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu
340	345	350
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr
355	360	365
Ile His His Ile Met Gly	Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp
370	375	380
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe	Glu Gln
385	390	395

&lt;210&gt; 495

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 414 GCG GCT

&lt;400&gt; 495

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	1	5	10	15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	20	25	30	
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	35	40	45	
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	50	55	60	

Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn 140	Gly	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val 190	Ala	Gln	His
Leu	Thr	His 195	Val	Ala	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr
Met 225	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys
Ile	Met	Ser 275	Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Gln
Pro	Val 290	Glu	Asp	Ile	Ser	Ser 295	Asn	Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro
Phe	Tyr	Gly 355	Cys	Val	Asn	Trp	Thr 360	Asn	Glu	Asn	Phe	Pro 365	Phe	Asn	Asp
Cys	Val 370	Asp	Lys	Met	Val	Ile 375	Trp	Trp	Glu	Glu	Gly 380	Lys	Met	Thr	Ala
Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Ala	Pro 415	Val
Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser
Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln
Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480
Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Pro 495	Ala
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val
Ala	Gln	Pro 515	Ser	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	Asp
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu								

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<210> 496  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 197 414 GCG GCT

<400> 496  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
                   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
                   180                  185                  190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                   195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
                   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
                   305                  310

<210> 497  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 30 54 127 GCG GCC GCT

<400> 497  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
   1                  5                  10                  15

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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Ala	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Ala	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val



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			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		580						585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	595						600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 498

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 30 54 127 GCG GCC GCT

&lt;400&gt; 498

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1			5					10						15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Ala	Ala	Glu		
		20						25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
	35						40					45					
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55				60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
		100						105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Ala	Leu		
	115						120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145					150					155				160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165					170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
		180					185						190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
	195					200						205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210				215						220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235				240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245					250						255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		260					265						270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275					280					285					

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 499

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 29 260 GCG GCG

&lt;400&gt; 499

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Ala	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 500

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<211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 29 260 GCG GCG

<400> 500  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 501  
 <211> 536

-584-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 29 260 GCG GCG

&lt;400&gt; 501

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Ala	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215						220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Ala	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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&lt;210&gt; 502

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 29 260 GCG GCG

&lt;400&gt; 502

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 503  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 4 484 GCT GCC

<400> 503  
 Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380



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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610          615          620

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&lt;210&gt; 504

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant-rep protein: rep52 4 484 GCT GCC

&lt;400&gt; 504

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Ala	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 505

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 4 484 GCT GCC

&lt;400&gt; 505

Thr	Ala	Gly	Ala	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	

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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 506

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 4 484 GCT GCC

&lt;400&gt; 506

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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[illegible]

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<210> 507
<211> 621
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mutant rep protein: rep78 258 124 132 GCC GCC GCC
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<400> 507															
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ala	Glu	Pro	Thr	Leu
		115					120					125			

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Pro	Asn	Trp	Ala	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195				200						205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250						255	
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275				280						285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345						350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	355						360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420				425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535						540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				

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610 615 620

<210> 508  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 258 124 132 GCC GCC GCC

<400> 508  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

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<210> 509  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 258 124 132 GCC GCC GCC

<400> 509

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ala	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Ala	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	



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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

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<210> 510  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 258 124 132 GCC GCC GCC

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<400> 510
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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[illegible]

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<220>
<223> Mutant rep protein: rep78 231 497 GCC GCC
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<400>	511															
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1				5					10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
			20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105						110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165				170						175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330							

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Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
370						375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
450						455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485				490						495	
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
530						535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
610						615					620				

&lt;210&gt; 512

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 231 497 GCC GCC

&lt;400&gt; 512

Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
50					55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85				90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
130						135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala

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145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275				280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290				295					300					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310						315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325					330						335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340						345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355				360					365				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370				375						380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 513

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 231 497 GCC GCC

&lt;400&gt; 513

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35				40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65				70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115				120						125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
530 535

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&lt;210&gt; 514

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 231 497 GCC GCC

&lt;400&gt; 514

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Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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			20				25				30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85						90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 515

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 221 258 GCA GCC

&lt;400&gt; 515

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		

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Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp



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595                      600                      605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
       610                      615                      620

<210> 516  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 221 258 GCA GCC

<400> 516  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   20                  25                  30  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                   180                  185                  190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                   195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Ala Lys Lys Arg Pro Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
   305                  310                  315                  320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
                   325                  330                  335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                   340                  345                  350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                   355                  360                  365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
                   370                  375                  380

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 517  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 221 258 GCA GCC

<400> 517  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 518

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 258 GCA GCC

&lt;400&gt; 518

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185				190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
                   305                  310

<210> 519  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 234 264 326 GCG GCG GCC

<400> 519  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
   1                  5                  10                  15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                  25                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                  40                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
                   50                  55                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
                   65                  70                  75                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                  90                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                  105                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
                   115                  120                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
                   130                  135                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
                   145                  150                  155                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                  170                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                  185                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                  200                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
                   210                  215                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys  
                   225                  230                  235                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   245                  250                  255  
 Ser Asn Ser Arg Ser Gln Ile Ala Ala Leu Asp Asn Ala Gly Lys  
                   260                  265                  270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   275                  280                  285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   290                  295                  300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   305                  310                  315                  320  
 Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   325                  330                  335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

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Phe	Tyr	Gly	340	Val	Asn	Trp	Thr	345	Asn	Glu	Asn	Phe	Pro	350	Phe	Asn	Asp
		355	Cys	Met	Val	Ile	Trp	360	Trp	Glu	Glu	Gly	365	Lys	Met	Thr	Ala
Cys	Val	Asp	Lys			375						380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
				405					410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
		450				455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
				485					490					495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530				535						540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
				565					570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln						
		610				615				620							

&lt;210&gt; 520

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 234 264 326 GCG GCG GCC

&lt;400&gt; 520

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Ala	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20				25						30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Ala	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35				40						45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65				70				75						80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85			90							95	
Thr	Lys	Lys	Phe	Gly	Ala	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 521

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 234 264 326 GCG GCG GCC

&lt;400&gt; 521

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

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130	Asn	Lys	Val	Val	Asp	Glu	135	Cys	Tyr	Ile	Pro	Asn	140	Tyr	Leu	Leu	Pro	Lys
145	Thr	Gln	Pro	Glu	Leu	Gln	150	Trp	Ala	Trp	Thr	155	Asn	Met	Glu	Gln	Tyr	Leu
						165						170						
	Ser	Ala	Cys	Leu	Asn	Leu		Thr	Glu	Arg	Lys		Arg	Leu	Val	Ala	Gln	His
						180						185						
	Leu	Thr	His	Val	Ser	Gln		Thr	Gln	Glu	Gln		Asn	Lys	Glu	Asn	Gln	Asn
						195						200						
	Pro	Asn	Ser	Asp	Ala	Pro		Val	Ile	Arg	Ser		Lys	Thr	Ser	Ala	Arg	Tyr
						210						215						
	Met	Glu	Leu	Val	Gly	Trp		Leu	Val	Asp	Ala		Gly	Ile	Thr	Ser	Glu	Lys
						225						230						
	Gln	Trp	Ile	Gln	Glu	Asp		Gln	Ala	Ser	Tyr		Ile	Ser	Phe	Asn	Ala	Ala
						245						250						
	Ser	Asn	Ser	Arg	Ser	Gln		Ile	Ala	Ala	Ala		Leu	Asp	Asn	Ala	Gly	Lys
						260						265						
	Ile	Met	Ser	Leu	Thr	Lys		Thr	Ala	Pro	Asp		Tyr	Leu	Val	Gly	Gln	Gln
						275						280						
	Pro	Val	Glu	Asp	Ile	Ser		Ser	Asn	Arg	Ile		Tyr	Lys	Ile	Leu	Glu	Leu
						290						295						
	Asn	Gly	Tyr	Asp	Pro	Gln		Tyr	Ala	Ala	Ser		Val	Phe	Leu	Gly	Trp	Ala
						305						310						
	Thr	Lys	Lys	Phe	Gly	Ala		Arg	Asn	Thr	Ile		Trp	Leu	Phe	Gly	Pro	Ala
						325						330						
	Thr	Thr	Gly	Lys	Thr	Asn		Ile	Ala	Glu	Ala		Ile	Ala	His	Thr	Val	Pro
						340						345						
	Phe	Tyr	Gly	Cys	Val	Asn		Trp	Thr	Asn	Glu		Asn	Phe	Pro	Phe	Asn	Asp
						355						360						
	Cys	Val	Asp	Lys	Met	Val		Ile	Trp	Trp	Glu		Glu	Gly	Lys	Met	Thr	Ala
						370						375						
	Lys	Val	Val	Glu	Ser	Ala		Lys	Ala	Ile	Leu		Gly	Gly	Ser	Lys	Val	Arg
						385						390						
	Val	Asp	Gln	Lys	Cys	Lys		Ser	Ser	Ala	Gln		Ile	Asp	Pro	Thr	Pro	Val
						405						410						
	Ile	Val	Thr	Ser	Asn	Thr		Asn	Met	Cys	Ala		Val	Ile	Asp	Gly	Asn	Ser
						420						425						
	Thr	Thr	Phe	Glu	His	Gln		Gln	Pro	Leu	Gln		Asp	Arg	Met	Phe	Lys	Phe
						435						440						
	Glu	Leu	Thr	Arg	Arg	Leu		Asp	His	Asp	Phe		Gly	Lys	Val	Thr	Lys	Gln
						450						455						
	Glu	Val	Lys	Asp	Phe	Phe		Arg	Trp	Ala	Lys		Asp	His	Val	Val	Glu	Val
						465						470						
	Glu	His	Glu	Phe	Tyr	Val		Lys	Lys	Gly	Gly		Ala	Lys	Lys	Arg	Pro	Ala
						485						490						
	Pro	Ser	Asp	Ala	Asp	Ile		Ser	Glu	Pro	Lys		Arg	Val	Arg	Glu	Ser	Val
						500						505						
	Ala	Gln	Pro	Ser	Thr	Ser		Asp	Ala	Glu	Ala		Ser	Ile	Asn	Tyr	Ala	Asp
						515						520						
	Arg	Leu	Ala	Arg	Gly	His		Ser	Leu									
						530						535						

&lt;210&gt; 522

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 234 264 326 GCG GCG GCC

&lt;400&gt; 522



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Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290     295     300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 523

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 153 398 AGC GCG

&lt;400&gt; 523

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

```

				85				90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ser	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150						155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Ala	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435													

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Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 524

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 153 398 AGC GCG

&lt;400&gt; 524

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Ala	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr

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		355					360					365				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
	370					375					380					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
385					390					395						

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<210> 525
<211> 536
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mutant rep protein: rep68 153 398 AGC GCG
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<400> 525																
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1				5					10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
			20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ser	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330				</			

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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 526

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 153 398 AGC GCG

&lt;400&gt; 526

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 527

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 53 216 GCG GCC

&lt;400&gt; 527

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Ala	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ala	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320

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Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 528

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 53 216 GCG GCC

&lt;400&gt; 528

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Ala	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile



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Arg	Glu	Lys	100	Leu	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	Glu	110	Pro	Thr	Leu
		115						120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
	130					135					140							
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
			165						170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185						190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ala	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245						250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265						270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280						285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325						330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 529

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 22 382 GCT GCG

&lt;400&gt; 529

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5				10						15	
Glu	His	Leu	Pro	Gly	Ala	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85				90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165				170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Ala	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln

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450		455		460
Glu Val Lys Asp Phe	Phe Arg Trp Ala Lys Asp His Val Val Glu Val			
465	470	475		480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala				
	485	490		495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val				
	500	505		510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp				
	515	520		525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu				
	530	535		540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys				
545	550	555		560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu				
	565	570		575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr				
	580	585		590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp				
	595	600		605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln				
610	615	620		

&lt;210&gt; 530

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 22 382 GCT GCG

&lt;400&gt; 530

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
	85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
	100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	
	115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	
	130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala	
145	150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	
	165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val	
	180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	
	195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	
	210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	
225	230
	235
	240

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 531

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 22 382 GCT GCG

&lt;400&gt; 531

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

				245				250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290				295						300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Ala	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

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<220>
<223> Mutant rep protein: rep40 22 382 GCT GCG
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<400> 532																
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
50					55						60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85						90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 533

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 231 411 GCC GCA

&lt;400&gt; 533

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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Pro	Asn	195	Ser	Asp	Ala	Pro	Val	200	Ile	Arg	Ser	Lys	Thr	205	Ser	Ala	Arg	Tyr
	210						215						220					
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
			275				280						285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325				330						335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp	Pro	Thr	Pro	Val			
				405				410						415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
				485				490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu			
	530					535					540							
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys			
545					550					555					560			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu			
				565				570						575				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr			
			580					585					590					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
		595					600					605						
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln							
	610					615				620								

&lt;210&gt; 534

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 231 411 GCC GCA



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<400> 534
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 535

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 231 411 GCC GCA

&lt;400&gt; 535

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Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130				135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala

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Pro	Ser	Asp	Ala	485	Ile	Ser	Glu	Pro	490	Lys	Arg	Val	Arg	Glu	495	Ser	Val
			500	Asp				505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515				520						525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

<210> 536  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 231 411 GCC GCA

Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
		20						25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55						60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130				135						140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp	Pro	Thr	Pro	Val
		180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260					265						270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275				280						285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290				295						300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

<210> 537  
 <211> 621  
 <212> PRT

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 59 305 GCG GCC

&lt;400&gt; 537

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Ala	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75						80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150				155						160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185				190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230					235						240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250						255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Ala	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

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		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 538

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 59 305 GCG GCC

&lt;400&gt; 538

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75					80		
Ala	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135				140							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195				200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 539

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 59 305 GCG GCC

&lt;400&gt; 539

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250				255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265				270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280				285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295				300				
Ala	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
		340					345					350		Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355					360					365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405					410					415	Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420					425					430		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440				445			Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455				460				Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490					495	Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		500					505					510		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520					525			Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 540

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 59 305 GCG GCC

&lt;400&gt; 540

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
		20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Ala	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85				90						95		



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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 541

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 53 231 GCG GCC

&lt;400&gt; 541

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405				410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530														

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<210> 542
<211> 397
<212> PRT
<213> Artificial Sequence
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&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 53 231 GCG GCC

&lt;400&gt; 542

Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260				265						270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275				280						285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305				310						315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325					330				335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340				345						350			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355				360						365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370				375						380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385				390						395					

&lt;210&gt; 543

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;223&gt; Mutant rep protein: rep68 53 231 GCG GCC

&lt;400&gt; 543

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Ala	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

<210> 544  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 53 231 GCG GCC

<400> 544  
 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

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<210> 545  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 258 498 GCC GCT

<400> 545  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

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&lt;210&gt; 546

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep proteinrep 52 258 498 GCC GCT

&lt;400&gt; 546

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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		195					200				205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ala	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His		Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 547

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 258 498 GCC GCT

&lt;400&gt; 547

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180					185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 245 250 255
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 485 490 495
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 515 520 525
Arg Leu Ala Arg Gly His Ser Leu
530 535

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&lt;210&gt; 548

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 258 498 GCC GCT

&lt;400&gt; 548

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1 5 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20 25 30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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65					70					75				80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
				85					90					95
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			100					105					110	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
		115					120					125		Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	130					135					140			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
145					150					155				Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
				165					170					Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
		180						185				190		Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		195					200					205		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	210					215					220			Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
225					230					235				Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
				245					250					Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			260					265					270	Ala
Pro	Ala	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		275					280					285		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	290					295					300			Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
305					310									

&lt;210&gt; 549

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 88 231 GCC GCC

&lt;400&gt; 549

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Ala	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160

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Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615						620			

&lt;210&gt; 550

&lt;211&gt; 397

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 88 231 GCC GCC

&lt;400&gt; 550

Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 551

&lt;211&gt; 536

&lt;212&gt; PRT

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 88 231 GCC GCC

&lt;400&gt; 551

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Ala	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

[illegible]

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<220>
<223> Mutant rep protein: rep40 88 231 GCC GCC
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<400>	552															
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
50						55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145				150					155						160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
	195						200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	290					295					300					



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Arg Leu Ala Arg Gly His Ser Leu  
305 310

<210> 553

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 101 363 GCA GCC

<400> 553

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Ala	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Ala	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg

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385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440				445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455				460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565					570						575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 554

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 101 363 GCA GCC

&lt;400&gt; 554

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Ala	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

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&lt;210&gt; 555

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 101 363 GCA GCC

&lt;400&gt; 555

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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			180					185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
225					230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245					250						255			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
			260					265						270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	275						280						285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			325					330						335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		340						345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Ala	Phe	Pro	Phe	Asn	Asp		
	355						360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		420					425						430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	435						440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		500					505						510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	515					520						525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

&lt;210&gt; 556

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 101 363 GCA GCC

&lt;400&gt; 556

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20				25						30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35						40						45		

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

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&lt;210&gt; 557

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 354 132 GCC GCC

&lt;400&gt; 557

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

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130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
	210	215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
	290	295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620

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<210> 558  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 354 132 GCC GCC

<400> 558  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 559



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<211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 354 132 GCC GCC

<400> 559  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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			420					425				430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		500					505						510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 560

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 354 132 GCC GCC

&lt;400&gt; 560

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20				25						30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Ala	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165						170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
	195					200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245						250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 561  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 10 132 GCG GCC

<400> 561  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Ala Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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370		375		380
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly	Gly Ser Lys Val Arg		
385	390	395	400	
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile	Asp Pro Thr Pro Val		
	405	410	415	
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val	Ile Asp Gly Asn Ser		
	420	425	430	
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp	Arg Met Phe Lys Phe		
	435	440	445	
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly	Lys Val Thr Lys Gln		
	450	455	460	
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp	His Val Val Glu Val		
465	470	475	480	
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala	Lys Lys Arg Pro Ala		
	485	490	495	
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg	Val Arg Glu Ser Val		
	500	505	510	
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser	Ile Asn Tyr Ala Asp		
	515	520	525	
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly	Met Asn Leu Met Leu		
	530	535	540	
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln	Asn Ser Asn Ile Cys		
545	550	555	560	
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys	Phe Pro Val Ser Glu		
	565	570	575	
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr	Gln Lys Leu Cys Tyr		
	580	585	590	
Ile His His Ile Met Gly	Lys Val Pro Asp Ala	Cys Thr Ala Cys Asp		
	595	600	605	
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe	Glu Gln		
610	615	620		

&lt;210&gt; 562

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 10 132 GCG GCC

&lt;400&gt; 562

Thr Ala Gly Phe Tyr Glu	Ile Val Ile Ala Val	Pro Ser Asp Leu Asp
1	5	10
Glu His Leu Pro Gly Ile	Ser Asp Ser Phe Val	Asn Trp Val Ala Glu
	20	25
Lys Glu Trp Glu Leu Pro	Pro Asp Ser Asp Met	Asp Leu Asn Leu Ile
	35	40
Glu Gln Ala Pro Leu Thr	Val Ala Glu Lys Leu	Gln Arg Asp Phe Leu
	50	55
Thr Glu Trp Arg Arg Val	Ser Lys Ala Pro Glu	Ala Leu Phe Phe Val
65	70	75
Gln Phe Glu Lys Gly Glu	Ser Tyr Phe His Met	His Val Leu Val Glu
	85	90
Thr Thr Gly Val Lys Ser	Met Val Leu Gly Arg	Phe Leu Ser Gln Ile
	100	105
Arg Glu Lys Leu Ile Gln	Arg Ile Tyr Arg Gly	Ile Glu Pro Thr Leu
	115	120
Pro Asn Trp Ala Ala Val	Thr Lys Thr Arg Asn	Gly Ala Gly Gly Gly
	130	135
Asn Lys Val Val Asp Glu	Cys Tyr Ile Pro Asn	Tyr Leu Leu Pro Lys
145	150	155

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Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185						190	
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 563

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 4 GCT

&lt;400&gt; 563

acggcggggg	cttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180

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cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggcct	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccca	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gaccgcgcc	cagtgcgca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcca	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	agacaaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 564

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant \_rep DNA sequence: 10 GCG

&lt;400&gt; 564

acggcggggt	tttacgagat	tgtgattgag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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-656-

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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 565

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 20 GCC

&lt;400&gt; 565

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ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 566

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



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&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 22 GCT

&lt;400&gt; 566

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cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 567

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 GCG

&lt;400&gt; 567

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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
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cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 568

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 38 GCG

&lt;400&gt; 568

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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
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cactctctct ga

1932

<210> 569  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 39 GCA

<400> 569  
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
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taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540  
aatctcacgg agcgtaaacg gttgggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
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cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780  
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ccagacgctt gcactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860  
caataaatga tttaaatcag gtatgggtgc cgatgggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

<210> 570  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 53 GCT

<400> 570  
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tctgacatgg atctgaatct gattgagcag gcacccgcta ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
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aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420

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gccggaggcg	ggaacaaggt	ggtggatgag	tgtacatcc	ccaattactt	gctcccaaaa	480
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aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggcct	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgttttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgtacatatt	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 571

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 59 GCG

&lt;400&gt; 571

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaaggcgag	180
cgcgactttc	tgacggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgca	1500



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gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccttg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 572

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 64 GCT

&lt;400&gt; 572

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttg	ctacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	ggttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	cgaaggctcg	ggagtcggcc	aaagccattc	tcggagggaag	caagggtgcg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 573

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 74 GCG

&lt;400&gt; 573

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acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 574

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 86 GCG

&lt;400&gt; 574

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagcgag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
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cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080

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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 575

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 88 GCC

&lt;400&gt; 575

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	cgtgggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	cgccttccac	atgcacgtgc	tcgtggaac	caccgggggtg	300
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgtactac	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttgaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
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gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 576

&lt;211&gt; 1932



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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 101 GCA

&lt;400&gt; 576

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ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 577

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 124 GCC

&lt;400&gt; 577

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-665-

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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 578

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 125 GCG

&lt;400&gt; 578

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caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 579  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 127 GCT

<400> 579						
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cactctctct	ga					1932

<210> 580  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 132 GCC

<400> 580						
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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

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caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tgggcccgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 581

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 140 GCC

&lt;400&gt; 581

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cactctctct	ga					1932

&lt;210&gt; 582

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 161 GCC

&lt;400&gt; 582

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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
gccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggaatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccega	ctcccgtgat	cgtcacctcc	1260
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gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 583

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-669-

&lt;223&gt; Mutant rep DNA sequence: 163 GCT

&lt;400&gt; 583

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ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccaggctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaaaccggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgthtttagag	tgctttcccg	tgctcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 584

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 175 GCT

&lt;400&gt; 584

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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	aggctttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900

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at t t t t g g a a c	t a a a c g g g t a	c g a t c c c c a a	t a t g c g g c t t	c c g t c t t t c t	g g g a t g g g c c	960
a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
a a t g a g a a c t	t t c c c t t c a a	c g a c t g t g t c	g a c a a g a t g g	t g a t c t g g t g	g g a g g a g g g g	1140
a a g a t g a c c g	c c a a g g t c g t	g g a g t c g g c c	a a a g c c a t t c	t c g g a g g a a g	c a a g g t g c g c	1200
g t g g a c c a g a	a a t g c a a g t c	c t c g g c c c a g	a t a g a c c c g a	c t c c c g t g a t	c g t c a c c t c c	1260
a a c a c c a a c a	t g t g c g c c g t	g a t t g a c g g g	a a c t c a a c g a	c c t t c g a a c a	c c a g c a g c c g	1320
t t g c a a g a c c	g g a t g t t c a a	a t t t g a a c t c	a c c c g c c g t c	t g g a t c a t g a	c t t t g g g a a g	1380
g t c a c c a a g c	a g g a a g t c a a	a g a c t t t t t c	c g g t g g g c a a	a g g a t c a c g t	g g t t g a g g t g	1440
g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g a c g c a	1500
g a t a t a a g t g	a g c c c a a a c g	g g t g c g c g a g	t c a g t t g c g c	a g c c a t c g a c	g t c a g a c g c g	1560
g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a c a a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932

&lt;210&gt; 585

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 193 GCG

&lt;400&gt; 585

a c g g c g g g g t	t t t a c g a g a t	t g t g a t t a a g	g t c c c c a g c g	a c c t t g a c g a	g c a t c t g c c c	60
g g c a t t t t c t g	a c a g c t t t g t	g a a c t g g g t g	g c c g a g a a g g	a a t g g g a g t t	g c c g c c a g a t	120
t c t g a c a t g g	a t c t g a a t c t	g a t t g a g c a g	g c a c c c c t g a	c c g t g g c c g a	g a a g c t g c a g	180
c g c g a c t t t c	t g a c g g a a t g	g c g c c g t g t g	a g t a a g g c c c	c g g a g g c c c t	t t t c t t t g t g	240
c a a t t t g a g a	a g g g a g a g a g	c t a c t t c c a c	a t g c a c g t g c	t c g t g g a a a c	c a c c g g g g t g	300
a a a t c c a t g g	t t t t g g g a c g	t t t c c t g a g t	c a g a t t c g c g	a a a a a c t g a t	t c a g a g a a t t	360
t a c c g c g g g a	t c g a g c c g a c	t t t g c c a a a c	t g g t t c g c g g	t c a c a a a g a c	c a g a a a t g g c	420
g c c g g a g g c g	g g a a c a a g g t	g g t g g a t g a g	t g c t a c a t c c	c c a a t t a c t t	g c t c c c c a a a	480
a c c c a g c c t g	a g c t c c a g t g	g g c g t g g a c t	a a t a t g g a a c	a g t a t t t a a g	c g c c t g t t t g	540
a a t c t c a c g g	a g c g t a a a c g	g t t g g t g g c g	c a g c a t g c g a	c g c a c g t g t c	g c a g a c g c a g	600
g a g c a g a a c a	a a g a g a a t c a	g a a t c c c a a t	t c t g a t g c g c	c g g t g a t c a g	a t c a a a a a c t	660
t c a g c c a g g t	a c a t g g a g c t	g g t c g g g t g g	c t c g t g g a c a	a g g g g a t t a c	c t c g g a g a a g	720
c a g t g g a t c c	a g g a g g a c c a	g g c c t c a t a c	a t c t c c t t c a	a t g c g g c c t c	c a a c t c g c g g	780
t c c c a a a t c a	a g g c t g c c t t	g g a c a a t g c g	g g a a a g a t t a	t g a g c c t g a c	t a a a a c c g c c	840
c c c g a c t a c c	t g g t g g g c c a	g c a g c c c g t g	g a g g a c a t t t	c c a g c a a t c g	g a t t t a t a a a	900
a t t t t g g a a c	t a a a c g g g t a	c g a t c c c c a a	t a t g c g g c t t	c c g t c t t t c t	g g g a t g g g c c	960
a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
a a t g a g a a c t	t t c c c t t c a a	c g a c t g t g t c	g a c a a g a t g g	t g a t c t g g t g	g g a g g a g g g g	1140
a a g a t g a c c g	c c a a g g t c g t	g g a g t c g g c c	a a a g c c a t t c	t c g g a g g a a g	c a a g g t g c g c	1200
g t g g a c c a g a	a a t g c a a g t c	c t c g g c c c a g	a t a g a c c c g a	c t c c c g t g a t	c g t c a c c t c c	1260
a a c a c c a a c a	t g t g c g c c g t	g a t t g a c g g g	a a c t c a a c g a	c c t t c g a a c a	c c a g c a g c c g	1320
t t g c a a g a c c	g g a t g t t c a a	a t t t g a a c t c	a c c c g c c g t c	t g g a t c a t g a	c t t t g g g a a g	1380
g t c a c c a a g c	a g g a a g t c a a	a g a c t t t t t c	c g g t g g g c a a	a g g a t c a c g t	g g t t g a g g t g	1440
g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g a c g c a	1500
g a t a t a a g t g	a g c c c a a a c g	g g t g c g c g a g	t c a g t t g c g c	a g c c a t c g a c	g t c a g a c g c g	1560
g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a a c a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932



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<210> 586  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 196 GCC

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acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tgggtcgcgg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgcctc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
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acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020  
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gtggaccaga aatgcaagtc ctcgccccag atagaccga ctcccgtgat cgtcacctcc 1260  
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
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gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg 1620  
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680  
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgcagaatc tcaaccggtt 1740  
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caataaatga tttaaatcag gtatgggtgc cgatgggttat cttccagatt ggctcgagga 1920  
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<210> 587  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 197 GCC

<400> 587  
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tgggtcgcgg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540

-672-

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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
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&lt;210&gt; 588

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 GCA

&lt;400&gt; 588

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtattttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
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cactctctct	ga					1932

&lt;210&gt; 589

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 228 GCG

&lt;400&gt; 589

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cactctctct	ga					1932

&lt;210&gt; 590

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 231 GCC

&lt;400&gt; 590

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&lt;210&gt; 591

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 234 GCG

&lt;400&gt; 591

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&lt;210&gt; 592

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 237 GCC

&lt;400&gt; 592

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tcccaaataca	aggctgcctt	ggacaatgcy	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 593

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 250 GCC

&lt;400&gt; 593

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	ggtgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 594

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 GCC

&lt;400&gt; 594

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840



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cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 595

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 260 GCG

&lt;400&gt; 595

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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tcagccagg	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcggcg	780
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cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920

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cactctctct ga

1932

<210> 596  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 263 GCC

<400> 596  
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ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg ggcgcgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540  
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcgagagaag 720  
cagtggatcc aggaggacca ggcctcatac atctccttca atggcgccct caactcgcg 780  
tcccaagcca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840  
cccactacc tggtagggcca gcagcccggt gaggacattt ccagcaatcg gatttataaa 900  
attttggaaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggccc 960  
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020  
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aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
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gatataagt agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
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cactctctct ga 1932

<210> 597  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 264 GCG

<400> 597  
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ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg ggcgcgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatcg	cggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atcttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 598

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 334 GCG

&lt;400&gt; 598

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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 599

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 335 GCT

&lt;400&gt; 599

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 600

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 337 GCT

&lt;400&gt; 600



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acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 601

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 341 GCC

&lt;400&gt; 601

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcagc	taccgggaag	1020
gccaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080

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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 602

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 342 GCC

&lt;400&gt; 602

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatac	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaatacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 603

&lt;211&gt; 1932



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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 347 GCA

&lt;400&gt; 603

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 604

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 AAT

&lt;400&gt; 604

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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660

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cactctctct	ga					1932

&lt;210&gt; 605

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 GCT

&lt;400&gt; 605

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<210> 606  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 354 GCC

<400> 606						
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<210> 607  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 363 GCC

<400> 607						
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&lt;210&gt; 608

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 364 GCT

&lt;400&gt; 608

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&lt;210&gt; 609

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 367 GCC

&lt;400&gt; 609

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&lt;210&gt; 610

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-688-

&lt;223&gt; Mutant rep DNA sequence:370 GCC

&lt;400&gt; 610

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aatgagaact	ttcccttcaa	cgactgtgcc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
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caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 611

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:376 GCG

&lt;400&gt; 611

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tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
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caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
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at t t t t g g a a c	t a a a c g g g t a	c g a t c c c c a a	t a t g c g g c t t	c c g t c t t t c t	g g g a t g g g c c	960
a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
a a t g a g a a c t	t t c c c t t c a a	c g a c t g t g t c	g a c a a g a t g g	t g a t c g c g t g	g g a g g a g g g g	1140
a a g a t g a c c g	c c a a g g t c g t	g g a g t c g g c c	a a a g c c a t t c	t c g g a g g a a g	c a a g g t g c g c	1200
g t g g a c c a g a	a a t g c a a g t c	c t c g g c c c a g	a t a g a c c c g a	c t c c c g t g a t	c g t c a c c t c c	1260
a a c a c c a a c a	t g t g c g c c g t	g a t t g a c g g g	a a c t c a a c g a	c c t t c g a a c a	c c a g c a g c c g	1320
t t g c a a g a c c	g g a t g t t c a a	a t t t g a a c t c	a c c c g c c g t c	t g g a t c a t g a	c t t t g g g a a g	1380
g t c a c c a a g c	a g g a a g t c a a	a g a c t t t t t c	c g g t g g g c a a	a g g a t c a c g t	g g t t g a g g t g	1440
g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g a c g c a	1500
g a t a t a a g t g	a g c c c a a a c g	g g t g c g c g a g	t c a g t t g c g c	a g c c a t c g a c	g t c a g a c g c g	1560
g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a a c a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932

&lt;210&gt; 612

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 381 GCG

&lt;400&gt; 612

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g g c a t t t c t g	a c a g c t t t g t	g a a c t g g g t g	g c c g a g a a g g	a a t g g g a g t t	g c c g c c a g a t	120
t c t g a c a t g g	a t c t g a a t c t	g a t t g a g c a g	g c a c c c c t g a	c c g t g g c c g a	g a a g c t g c a g	180
c g c g a c t t t c	t g a c g g a a t g	g c g c c g t g t g	a g t a a g g c c c	c g g a g g c c c t	t t t c t t t g t g	240
c a a t t t g a g a	a g g g a g a g a g	c t a c t t c c a c	a t g c a c g t g c	t c g t g g a a a c	c a c c g g g g t g	300
a a a t c c a t g g	t t t t g g g a c g	t t t c c t g a g t	c a g a t t c g c g	a a a a a c t g a t	t c a g a g a a t t	360
t a c c g c g g g a	t c g a g c c g a c	t t t g c c a a a c	t g g t t c g c g g	t c a c a a a g a c	c a g a a a t g g c	420
g c c g g a g g c g	g g a a c a a g g t	g g t g g a t g a g	t g c t a c a t c c	c c a a t t a c t t	g c t c c c c a a a	480
a c c c a g c c t g	a g c t c c a g t g	g g c g t g g a c t	a a t a t g g a a c	a g t a t t t a a g	c g c c t g t t t g	540
a a t c t c a c g g	a g c g t a a a c g	g t t g g t g g c g	c a g c a t c t g a	c g c a c g t g t c	g c a g a c g c a g	600
g a g c a g a a c a	a a g a g a a t c a	g a a t c c c a a t	t c t g a t g c g c	c g g t g a t c a g	a t c a a a a a c t	660
t c a g c c a g g t	a c a t g g a g c t	g g t c g g g t g g	c t c g t g g a c a	a g g g g a t t a c	c t c g g a g a a g	720
c a g t g g a t c c	a g g a g g a c c a	g g c c t c a t a c	a t c t c c t t c a	a t g c g g c c t c	c a a c t c g c g g	780
t c c c a a a t c a	a g g c t g c c t t	g g a c a a t g c g	g g a a a g a t t a	t g a g c c t g a c	t a a a a c c g c c	840
c c c g a c t a c c	t g g t g g g c c a	g c a g c c c g t g	g a g g a c a t t t	c c a g c a a t c g	g a t t t a t a a a	900
a t t t t g g a a c	t a a a c g g g t a	c g a t c c c c a a	t a t g c g g c t t	c c g t c t t t c t	g g g a t g g g c c	960
a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
a a t g a g a a c t	t t c c c t t c a a	c g a c t g t g t c	g a c a a g a t g g	t g a t c t g g t g	g g a g g a g g g g	1140
g c g a t g a c c g	c c a a g g t c g t	g g a g t c g g c c	a a a g c c a t t c	t c g g a g g a a g	c a a g g t g c g c	1200
g t g g a c c a g a	a a t g c a a g t c	c t c g g c c c a g	a t a g a c c c g a	c t c c c g t g a t	c g t c a c c t c c	1260
a a c a c c a a c a	t g t g c g c c g t	g a t t g a c g g g	a a c t c a a c g a	c c t t c g a a c a	c c a g c a g c c g	1320
t t g c a a g a c c	g g a t g t t c a a	a t t t g a a c t c	a c c c g c c g t c	t g g a t c a t g a	c t t t g g g a a g	1380
g t c a c c a a g c	a g g a a g t c a a	a g a c t t t t t c	c g g t g g g c a a	a g g a t c a c g t	g g t t g a g g t g	1440
g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g a c g c a	1500
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g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a a c a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932

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<220>  
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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
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-691-

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&lt;210&gt; 615

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 407 GCC

&lt;400&gt; 615

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acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaaggc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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gatataagt	agcccaaacy	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620

-692-

aatctgatgc	tgtttcctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 616

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 411 GCA

&lt;400&gt; 616

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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gtcaccaagc	aggaagtcaa	agactttttc	cggtagggcaa	aggatcacgt	ggttgagggtg	1440
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gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 617

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 414 GCT

&lt;400&gt; 617

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120



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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggcct	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccggg	ctcccgtgat	cgtcacctcc	1260
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 618

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 420 GCT

&lt;400&gt; 618

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200

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gtggaccaga	aatgcaagtc	ctcggccccag	atagacccga	ctcccgtgat	cgtcaccgct	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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caataaatga	tttaaatacag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 619

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 421 GCC

&lt;400&gt; 619

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggccccag	atagacccga	ctcccgtgat	cgtcacctcc	1260
gccaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 620

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



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&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 422 GCC

&lt;400&gt; 620

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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gtcaccaagc	aggaagtcaa	agactthtttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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ttcactcacg	gacagaaaga	ctgthttagag	tgctthtccc	tgtcagaatc	tcaaccggtt	1740
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 621

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 424 GCG

&lt;400&gt; 621

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-696-

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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 622

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 428 GCT

&lt;400&gt; 622

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcgggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
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cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
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ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920

-697-

cactctctct ga

1932

&lt;210&gt; 623

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:429 GCC

&lt;400&gt; 623

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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cccgactacc	tggtgggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggccccag	atagacccega	ctcccgtgat	cgtcacctcc	1260
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 624

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 438 GCG

&lt;400&gt; 624

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 625

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 440 GCG

&lt;400&gt; 625

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
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cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggttggg	gccaaagaaa	gacccgcccc	cagtgcagca	1500



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gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 626

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 451 GCC

&lt;400&gt; 626

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 627

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 460 GCG

&lt;400&gt; 627

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 628

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 462 GCC

&lt;400&gt; 628

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080



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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 629

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 462 ATA

&lt;400&gt; 629

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgtgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
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cccgtacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaa	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtttg	ggcctgcaac	taccgggaag	1020
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 630

&lt;211&gt; 1932

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 484 GCC

&lt;400&gt; 630

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ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 631

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 488 GCG

&lt;400&gt; 631

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

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tcagccaggt	acatggagct	ggtcgggttg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
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caataaatga	thtaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 632

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 GCC

&lt;400&gt; 632

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcatttctg	acagctthgt	gaactgggtg	gcagagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactthc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	thctthgtg	240
caatttgaga	agggagagag	ctactthccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	thttgggacg	thtctgtagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gtcaccaagc	aggaagtcaa	agactthttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
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<210> 633  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 497 GCC

<400> 633						
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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<210> 634  
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<223> Mutant rep DNA sequence: 497 CGA

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caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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cactctctct	ga					1932

&lt;210&gt; 635

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 497 CTC

&lt;400&gt; 635

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cactctctct	ga					1932

&lt;210&gt; 636

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 497 TAC

&lt;400&gt; 636

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&lt;210&gt; 637

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;



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&lt;223&gt; Mutant rep DNA sequence: 498 GCT

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caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

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&lt;210&gt; 638

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:499 GCC

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cagtggatcc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg 780
tcccaaatac aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
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a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
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g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g c c g c a	1500
g a t a t a a g t g	a g c c c a a a c g	g g t g c g c g a g	t c a g t t g c g c	a g c c a t c g a c	g t c a g a c g c g	1560
g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a a c a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932

&lt;210&gt; 639

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 503 GCG

&lt;400&gt; 639

a c g g c g g g g t	t t t a c g a g a t	t g t g a t t a a g	g t c c c c a g c g	a c c t t g a c g a	g c a t c t g c c c	60
g g c a t t t c t g	a c a g c t t t g t	g a a c t g g g t g	g c c g a g a a g g	a a t g g g a g t t	g c c g c c a g a t	120
t c t g a c a t g g	a t c t g a a t c t	g a t t g a g c a g	g c a c c c c t g a	c c g t g g c c g a	g a a g c t g c a g	180
c g c g a c t t t c	t g a c g g a a t g	g c g c c g t g t g	a g t a a g g c c c	c g g a g g c c c t	t t t c t t t g t g	240
c a a t t t g a g a	a g g g a g a g a g	c t a c t t c c a c	a t g c a c g t g c	t c g t g g a a a c	c a c c g g g g t g	300
a a a t c c a t g g	t t t t g g g a c g	t t t c c t g a g t	c a g a t t c g c g	a a a a a c t g a t	t c a g a g a a t t	360
t a c c g c g g g a	t c g a g c c g a c	t t t g c c a a a c	t g g t t c g c g g	t c a c a a a g a c	c a g a a a t g g c	420
g c c g g a g g c g	g g a a c a a g g t	g g t g g a t g a g	t g c t a c a t c c	c c a a t t a c t t	g c t c c c c a a a	480
a c c c a g c c t g	a g c t c c a g t g	g g c g t g g a c t	a a t a t g g a a c	a g t a t t t a a g	c g c c t g t t t g	540
a a t c t c a c g g	a g c g t a a a c g	g t t g g t g g c g	c a g c a t c t g a	c g c a c g t g t c	g c a g a c g c a g	600
g a g c a g a a c a	a a g a g a a t c a	g a a t c c c a a t	t c t g a t g c g c	c g g t g a t c a g	a t c a a a a a c t	660
t c a g c a g g t	a c a t g g a g c t	g g t c g g g t g g	c t c g t g g a c a	a g g g g a t t a c	c t c g g a g a a g	720
c a g t g g a t c c	a g g a g g a c c a	g g c c t c a t a c	a t c t c c t t c a	a t g c g g c c t c	c a a c t c g c g g	780
t c c c a a a t c a	a g g c t g c c t t	g g a c a a t g c g	g g a a a g a t t a	t g a g c c t g a c	t a a a a c c g c c	840
c c c g a c t a c c	t g g t g g g c c a	g c a g c c c g t g	g a g g a c a t t t	c c a g c a a t c g	g a t t t a t a a a	900
a t t t t g g a a c	t a a a c g g g t a	c g a t c c c c a a	t a t g c g g c t t	c c g t c t t t c t	g g g a t g g g c c	960
a c g a a a a a g t	t c g g c a a g a g	g a a c a c c a t c	t g g c t g t t t g	g g c c t g c a a c	t a c c g g g a a g	1020
a c c a a c a t c g	c g g a g g c c a t	a g c c c a c a c t	g t g c c c t t c t	a c g g g t g c g t	a a a c t g g a c c	1080
a a t g a g a a c t	t t c c c t t c a a	c g a c t g t g t c	g a c a a g a t g g	t g a t c t g g t g	g g a g g a g g g g	1140
a a g a t g a c c g	c c a a g g t c g t	g g a g t c g g c c	a a a g c c a t t c	t c g g a g g a a g	c a a g g t g c g c	1200
g t g g a c c a g a	a a t g c a a g t c	c t c g g c c c a g	a t a g a c c c g a	c t c c c g t g a t	c g t c a c c t c c	1260
a a c a c c a a c a	t g t g c g c c g t	g a t t g a c g g g	a a c t c a a c g a	c c t t c g a a c a	c c a g c a g c c g	1320
t t g c a a g a c c	g g a t g t t c a a	a t t t g a a c t c	a c c c g c c g t c	t g g a t c a t g a	c t t t g g g a a g	1380
g t c a c c a a g c	a g g a a g t c a a	a g a c t t t t t c	c g g t g g g c a a	a g g a t c a c g t	g g t t g a g g t g	1440
g a g c a t g a a t	t c t a c g t c a a	a a a g g g t g g a	g c c a a g a a a a	g a c c c g c c c c	c a g t g a c g c a	1500
g a t a t a g c g g	a g c c c a a a c g	g g t g c g c g a g	t c a g t t g c g c	a g c c a t c g a c	g t c a g a c g c g	1560
g a a g c t t c g a	t c a a c t a c g c	a g a c a g g t a c	c a a a a c a a a t	g t t c t c g t c a	c g t g g g c a t g	1620
a a t c t g a t g c	t g t t t c c c t g	c a g a c a a t g c	g a g a g a a t g a	a t c a g a a t t c	a a a t a t c t g c	1680
t t c a c t c a c g	g a c a g a a a g a	c t g t t t a g a g	t g c t t t c c c g	t g t c a g a a t c	t c a a c c c g t t	1740
t c t g t c g t c a	a a a a g g c g t a	t c a g a a a c t g	t g c t a c a t t c	a t c a t a t c a t	g g g a a a g g t g	1800
c c a g a c g c t t	g c a c t g c c t g	c g a t c t g g t c	a a t g t g g a t t	t g g a t g a c t g	c a t c t t t g a a	1860
c a a t a a a t g a	t t t a a a t c a g	g t a t g g c t g c	c g a t g g t t a t	c t t c c a g a t t	g g c t c g a g g a	1920
c a c t c t c t c t	g a					1932

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<210> 640  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 510 GCA

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tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
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gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
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<210> 641  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 511 GCA

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tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540

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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
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&lt;210&gt; 642

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 512 GCT

&lt;400&gt; 642

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&lt;210&gt; 643

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 516 GCG

&lt;400&gt; 643

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ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 644

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 517 GCT

&lt;400&gt; 644

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120

-712-

tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtccggc	aaagccattc	tcggagggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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ttgcaagacc	ggatgttcaa	atthtgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
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gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcggc	ttcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 645

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant -rep DNA sequence: 517 AAC

&lt;400&gt; 645

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtccggc	aaagccattc	tcggagggaag	caagggtgcgc	1200



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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
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gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgaa	ctcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 646

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 518 GCA

&lt;400&gt; 646

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgacag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatac	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgtactac	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtcggcc	aaagccattc	tcggaggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
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gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 647

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 519 GCG

&lt;400&gt; 647

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggcctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agacttttct	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagcggcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 648

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 598 GCA

&lt;400&gt; 648

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
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aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-715-

cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	ggcaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctthgaa	1860
caataaatga	thtaaatcag	gtatgggtgc	cgatgggttat	ctthccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 649

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 600 GCG

&lt;400&gt; 649

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattthctg	acagctthtgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttht	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	thtctthtgtg	240
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aaatccatgg	thttgggacg	thtctgtagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
thccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgccc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgca	1500
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gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctthgaa	1860
caataaatga	thtaaatcag	gtatgggtgc	cgatgggttat	ctthccagatt	ggctcgagga	1920

-716-

cactctctct ga

1932

&lt;210&gt; 650

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 601 GCA

&lt;400&gt; 650

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagg	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 651

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 335 420, 495 GCT GCC GCC

&lt;400&gt; 651

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-717-

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caataaatga tttaaatcag gtatggctgc cgatggttat ctccagatt ggctcgagga 1920
cactctctct ga 1932

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&lt;210&gt; 652

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 39 140 GCA GCC

&lt;400&gt; 652

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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacgggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
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-718-

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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 653

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 279 428 451 GCC GCT GCC

&lt;400&gt; 653

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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 654

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 125 237 600 GCG GCC GCG

&lt;400&gt; 654



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cactctctct	ga					1932

&lt;210&gt; 655

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 163 259 GCT GCG

&lt;400&gt; 655

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-720-

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gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 656

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 17 127 189 GCG GCT GCG

&lt;400&gt; 656

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacgc	gcattctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	gggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accgagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	ggtggcgggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	gggtcggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgccg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 657

&lt;211&gt; 1932

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 428 GCT GCT

&lt;400&gt; 657

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atttttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacgct	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
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gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 658

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 338 495 GCC GCC GCC

&lt;400&gt; 658

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

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tcagccaggt	acatggagct	ggtcgggttg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	tgccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
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gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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ctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 659

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 420 GCT GCC

&lt;400&gt; 659

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatcg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
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tcagccaggt	acatggagct	ggtcgggttg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacccgc	1260
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
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ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740



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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 660

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 189 197 518 GCG GCG GCA

&lt;400&gt; 660

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	ggcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgthtttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 661

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 468 516 GCC GCG

&lt;400&gt; 661

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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-724-

caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
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cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
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&lt;210&gt; 662

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 127 221 350 54 140 GCT

GCA GCT GCC GCC

&lt;400&gt; 662

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caataaatga	tttaaatacag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 663

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 285 GCA GCG

&lt;400&gt; 663

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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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caataaatga	tttaaatacag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 664

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 23 495 GCT GCC

&lt;400&gt; 664

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accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgcctgtttg	540
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caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
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&lt;210&gt; 665

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep DNA sequence: 20 54 420 495 GCC GCC GCC  
GCC

&lt;400&gt; 665

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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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cactctctct	ga					1932

&lt;210&gt; 666

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 412 612 GCC GCG

&lt;400&gt; 666

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cactctctct ga 1932

<210> 667  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 197 412 GCG GCC

<400> 667  
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cactctctct ga 1932

<210> 668  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 412 495 511 GCC GCC GCA

<400> 668  
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg ggcgctgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360



-729-

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	ggtgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 669

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 98 422 GCC GCC

&lt;400&gt; 669

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&lt;210&gt; 670

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 17 127 189 GCG GCT GCG

&lt;400&gt; 670

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cactctctct	ga					1932

&lt;210&gt; 671

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 20 54 495 GCC GCC GCC



-731-

<400> 671  
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caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

&lt;210&gt; 672

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 163 GCC GCT

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gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
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gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgagaca aggggattac ctccggagaag 720  
cagtggatcc aggaggacca ggcctcctac atctccttca atgcggcctc caactcgcg 780  
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-732-

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cactctctct	ga					1932

&lt;210&gt; 673

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 259 54 GCG GCC

&lt;400&gt; 673

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&lt;210&gt; 674

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&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 335 399 GCT GCG

&lt;400&gt; 674

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cactctctct	ga					1932

&lt;210&gt; 675

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 432 GCA GCA

&lt;400&gt; 675

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&lt;210&gt; 676

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 259 516 GCG GCG

&lt;400&gt; 676

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<210> 677  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 495 516 GCC GCG

<400> 677						
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<210> 678  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 414 14 GCT GCC

<400> 678						
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&lt;210&gt; 679

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 74 402 495 GCG GCC GCC

&lt;400&gt; 679

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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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gtggcccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260



-737-

aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 680

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 228 462 497 GCC GCC GCC

&lt;400&gt; 680

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggccgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 681

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-738-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 290 338 GCG GCC

&lt;400&gt; 681

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tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgctg	780
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cccgactacc	tggtgggcca	gcagcccgcg	gaggacattt	ccagcaatcg	gatttataaa	900
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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caataaatga	tttaaatcag	gtatgggtgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 682

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 140 511 GCC GCA

&lt;400&gt; 682

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatgcc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840

-739-

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caataaatga	thtaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 683

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 86 378 GCG GCG

&lt;400&gt; 683

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ggcatthtctg	acagctthtgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttht	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	thtctthtgtg	240
caatthtgaga	agggagcgag	ctactthcac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	thttgggacg	thtccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	thtgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatthtaag	cgcctgttht	540
aatctcacgg	agcgtaaacg	gthtgggtgg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctcctthca	atgcggccct	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgccc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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caataaatga	thtaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920

-740-

cactctctct ga

1932

&lt;210&gt; 684

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 86 GCC GCG

&lt;400&gt; 684

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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cccactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 685

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 214 495 140 GCG GCC GCC

&lt;400&gt; 685

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420



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gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgg	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgatcagaatc	tcaaccggtt	1740
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 686

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 511 GCC GCA

&lt;400&gt; 686

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
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aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
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gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gagccgcccc	cagtgcgca	1500

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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 687

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 54 GCC GCC

&lt;400&gt; 687

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
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tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 688

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 495 GCG GCC

&lt;400&gt; 688



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caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 689

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 261 20 GCC GCC

&lt;400&gt; 689

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctggcc	60
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tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 690

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 20 GCC GCC

&lt;400&gt; 690

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cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
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ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 691

&lt;211&gt; 1932

-745-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 420 GCG GCC

&lt;400&gt; 691

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgagg	780
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 692

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 338 495 GCC GCC GCC

&lt;400&gt; 692

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ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctthtga	1860
caataaatga	thtaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 693

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 427 GCG GCG

&lt;400&gt; 693

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgccc	60
ggcatttctg	acagctthtgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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taccgcggga	tcgagccgac	thtgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	gggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaa	agtattthaag	cgcctgttht	540
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cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 694

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep DNA sequence: 54 228 370 387 GCC GCC  
GCC GCC

&lt;400&gt; 694

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ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 695

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 289 GCA GCC

&lt;400&gt; 695

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-748-

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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
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&lt;210&gt; 696

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 163 GCC GCT

&lt;400&gt; 696

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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260



-749-

aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 697

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 341 407 420 GCC GCC GCC

&lt;400&gt; 697

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggcct	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
gccaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
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gtggaccaga	aatgcaaggc	ctcggccccag	atagaccgga	ctcccgtgat	cgtcaccgcc	1260
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gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 698

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-750-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 228 GCC GCC

&lt;400&gt; 698

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggccgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaa	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 699

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 96 125 511 GCA GCG GCA

&lt;400&gt; 699

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggcaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-751-

cccgactacc	tggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	ttaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gatataagtg	agcccaaacg	gggtgcgcgag	gcagttgcgc	agccatcgac	gtcagacgcg	1560
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 700

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 420 GCG GCC

&lt;400&gt; 700

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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aaatccatgg	ttttgggacg	tttctgtagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaaacaagg	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgcctgtttg	540
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	ttaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcaccgcc	1260
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gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
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gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920

-752-

cactctctct ga

1932

&lt;210&gt; 701

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 334 428 499 GCG GCT GCC

&lt;400&gt; 701

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	cgcttgcaac	taccgggaag	1020
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aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcccgtc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactthttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgccgca	1500
gatataagt	agcccaaacy	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgthttagag	tgctthtccc	tgctcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 702

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 414 GCG GCT

&lt;400&gt; 702

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420



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gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaag	gttggtggcg	cagcatctga	cgacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccggg	ctcccgtgat	cgtcacctcc	1260
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aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggt	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 703

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 30 54 127 GCG GCC GCT

&lt;400&gt; 703

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgccc	60
ggcattttctg	acagctttgt	gaactgggag	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaag	gttggtggcg	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
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gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
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tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 704

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 260 GCG GCG

&lt;400&gt; 704

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcatttctg	acagctttgt	gaacgcggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
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aatctcacgg	agcgtaaaac	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcggcg	780
tcccaaatca	aggctgcctt	ggacaatgcy	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccaact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
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gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 705

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 260 GCG GCG

&lt;400&gt; 705



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acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaacgcggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcggcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 706

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 4 484 GCT GCC

&lt;400&gt; 706

acggcggggg	cttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcggcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
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acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080

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gtggaccaga	aatgcaagtc	ctcgccccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 707

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 124 132 GCC GCC GCC

&lt;400&gt; 707

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ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
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acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtattttaag	cgctgttttg	540
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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	cgcctcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggcct	ccgtctttct	gggatggggcc	960
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gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
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caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 708

&lt;211&gt; 1932

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 231 497 GCC GCC

&lt;400&gt; 708

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ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
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&lt;210&gt; 709

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 258 GCA GCC

&lt;400&gt; 709

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&lt;210&gt; 710

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 234 264 326 GCG GCG GCC

&lt;400&gt; 710

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<210> 711  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 153 398 AGC GCG

<400> 711							
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<210> 712  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 53 216 GCG GCC

<400> 712							
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&lt;210&gt; 713

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 22 382 GCT GCG

&lt;400&gt; 713

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&lt;210&gt; 714

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 231 411 GCC GCA

&lt;400&gt; 714

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&lt;210&gt; 715

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-762-

&lt;223&gt; Mutant rep DNA sequence: 59 305 GCG GCC

&lt;400&gt; 715

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caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 716

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 53 231 GCG GCC

&lt;400&gt; 716

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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 717

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 498 GCC GCT

&lt;400&gt; 717

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<210> 718  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 88 231 GCC GCC

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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
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aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540  
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
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cactctctct ga 1932

<210> 719  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 101 363 GCA GCC

<400> 719  
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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
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gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540



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tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
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&lt;210&gt; 720

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 354 132 GCC GCC

&lt;400&gt; 720

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caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 721

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 10 132 GCG GCC

&lt;400&gt; 721

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cactctctct	ga					1932

&lt;210&gt; 722

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; intron 630 tgc gcg

&lt;400&gt; 722

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atgcgagaga	atgaatcaga	attcaaatat	ctgcttcact	cacggacaga	aagactgttt	120



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<220>  
 <223> intron 630 tgc cgc

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agagtgcctt	cccggtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	180
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 <213> Artificial Sequence

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 <223> intron 630 tgc cct

<400> 724						
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agagtgcctt	cccggtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	180
actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcaactg	cctgcgatct	240
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<210> 725  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> intron 630 tgc tca

<400> 725						
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actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcaactg	cctgcgatct	240
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<210> 726  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> mutant rep DNA sequence: 598 GAC

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<400> 726  
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cgcgactttc tgacggaatg gcgcccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420  
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cactctctct ga 1932

&lt;210&gt; 727

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 598 AGC

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cactctctct	ga					1932

&lt;210&gt; 728

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 600 CCG

&lt;400&gt; 728

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&lt;210&gt; 729

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<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> mutant rep DNA sequence: 630 GCG

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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
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taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
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-771-

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&lt;213&gt; Artificial Sequence

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&lt;400&gt; 731

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A61P 15/00, 31/18, 35/00

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(74) Agents: CABINET ORES et al.; 36, rue de St Péters-  
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GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,  
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WO 2003/018820 A3

(54) Title: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES RELATED APPLICATIONS

(57) Abstract: Mutant AAV REP proteins and their use in improving recombinant AAV production are provided.

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/IB 02/04087

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC 7 C12N15/864 C12N15/62 C12N15/35 C12N15/10 C12N7/01 C12N5/10 C07K14/015 C12Q1/70 A61P15/00 A61P31/18 A61P35/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N C07K C12Q A61P		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, Sequence Search, CHEM ABS Data, WPI Data, PAJ, BIOSIS, EMBASE		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 01/032711 A (TRUSTEES OF THE UNIVERSITY OF ;HERMONAT PAUL L (US)) 10 May 2001 (2001-05-10)  claims 11-18	1-11,13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88, 91-93
A	WO 01/025253 A (ABERNATHY CORINNE ;SAMULSKI RICHARD JUDE (US); UNIV NORTH CAROLINA) 12 April 2001 (2001-04-12) claims 6,8-11,53,54; table 1  ----- -/--	
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C.		
<input checked="" type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family		
Date of the actual completion of the international search  23 September 2003		Date of mailing of the international search report  04 02 2004
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer  Lonnoy, O

# INTERNATIONAL SEARCH REPORT

Internatl plication No  
PCT/IB 02/04087

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	URABE MASASHI ET AL: "Charged-to-alanine scanning mutagenesis of the N-terminal half of adeno-associated virus type 2 Rep78 protein" JOURNAL OF VIROLOGY, THE AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 73, no. 4, April 1999 (1999-04), pages 2682-2693, XP002164718 ISSN: 0022-538X	
A	----- WO 99/07833 A (CELL GENESYS INC) 18 February 1999 (1999-02-18)	
A	----- WO 98/13487 A (MAXYGEN INC) 2 April 1998 (1998-04-02) -----	

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 02/04087

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
  
Although claims 56 and 85-87, as far as they relate to methods practiced in vivo, are directed to methods of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
  
1-11, 13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88  
91-93 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-11, 13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88, 91-93 (all partially)

AAV Rep mutant protein exhibiting mutation at aa 4 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; said Rep mutant protein as represented by SeqIdNo1 (F4A Rep78) or SeqIdNo.2 (F4A Rep68); nucleic acid encoding said mutant Rep protein; said nucleic acid as represented by SeqIdNo.563; AAV comprising a nucleic acid encoding said mutant Rep protein; a fusion protein comprising said mutant Rep protein; pharmaceutical composition, production method and uses thereof.

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Inventions 2-86: claims 1-24 and 39-93 (all partially, as applicable)

As for invention 1, wherein invention 2 relates to amino and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 10 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; invention 3 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 20 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; invention 4 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 22 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; ...; invention 86 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 601 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype.

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Invention 87: claims 25-32 (all totally) and 1-5, 20-22, 43-56, 89-93 (all partially)

An AAV genome comprising a mutation at one or more nucleotides which encode amino acid residue 630 of AAV2 Rep78; corresponding protein, fusion protein, AAV, pharmaceutical composition, production method, and uses thereof.

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Invention 88: claim 33 (totally)

Method of titering a virus comprising incubating a host cell with a reporter virus and the virus to be probed, measuring the output signal of the reporter virus, and comparing the titer of the reporter virus in the presence and absence of the titering virus.



FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

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Invention 89: claims 34-38 (all totally)

Process for producing recombinant AAV or AAV protein having  
a predetermined property comprising characterisation and  
modification of "hit" positions, and identification of  
"lead" compounds.

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# INTERNATIONAL SEARCH REPORT

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Internati

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